SEQUENCE LISTING

<110> Steinbuchel, Alexander
      Priefert, Horst
      Rabenhorst, Jurgen

<120> SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL
      ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND
      VANILLIC ACID AND THEIR USE

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<140> 09/750,986
<141> 2000-12-28

<150> 196 49 655.1 GERMANY
<151> 1996-11-29

<160> 45

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<212> PRT
<213> Pseudomonas sp.

<400> 2

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             20                  25                  30

Arg Asp Pro Asn Lys Ala Gly Asp Leu Thr Ala Arg Gly Ile Val Val
         35                  40                  45

Arg Gln Ala Asp Tyr Asn Arg Pro Glu Thr Leu His Arg Ala Leu Ile
     50                  55                  60

Gly Val Asn Arg Leu Leu Leu Ile Ser Ser Ser Glu Val Gly Gln Arg
 65                  70                  75                  80

Thr Ala Gln His Arg Ala Val Ile Asp Ala Ala Lys Gln Glu Gly Ile
                 85                  90                  95

Glu Leu Leu Ala Tyr Thr Ser Leu Leu His Ala Asp Lys Ser Ala Leu
               100                 105                 110
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Gly Leu Ala Thr Glu His Arg Asp Thr Glu Gln Ala Leu Thr Glu Ser
    115   120   125

Gly Ile Pro His Val Leu Leu Arg Asn Gly Trp Tyr His Glu Asn Tyr
    130   135   140

Thr Ala Gly Ile Pro Val Ala Leu Val His Gly Val Leu Leu Gly Cys
145   150   155   160

Ala Gln Asp Gly Leu Ile Ala Ser Ala Ala Arg Ala Asp Tyr Ala Glu
                165   170   175

Ala Ala Ala Val Val Leu Thr Gly Glu Asn Gln Ala Gly Arg Val Tyr
            180   185   190

Glu Leu Ala Gly Glu Pro Ala Tyr Thr Leu Thr Glu Leu Ala Ala Glu
        195   200   205

Val Ala Pro Gln Ala Gly Lys Thr Val Val Tyr Ser Asn Leu Ser Glu
    210   215   220

Ser Asp Tyr Arg Ser Ala Leu Ile Ser Ala Gly Leu Pro Asp Gly Phe
225   230   235   240

Ala Ala Leu Leu Ala Asp Ser Asp Ala Gly Ala Ala Lys Gly Tyr Leu
            245   250   255

Phe Asp Ser Ser Gly Asp Ser Arg Lys Leu Ile Gly Arg Pro Thr Thr
            260   265   270

Pro Met Ser Glu Ala Ile Ala Ala Ala Ile Gly Arg
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<211> 1065
<212> DNA
<213> Pseudomonas sp.

<220>
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<223> product = "Vanillinsaeure-O-Demethylase" / gene =
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Met Phe Pro Lys Asn Ala Trp Tyr Val Ala Cys Thr Pro Asp Glu Ile
  1   5   10   15

gca gat aag ccg cta ggc cgt cag atc tgc aac gaa aag att gtc ttc   96
Ala Asp Lys Pro Leu Gly Arg Gln Ile Cys Asn Glu Lys Ile Val Phe
             20   25   30

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tat cgg ggg ccg gaa gga cgt gtt gcc gcg gta gag gat ttc tgc cct    144
Tyr Arg Gly Pro Glu Gly Arg Val Ala Ala Val Glu Asp Phe Cys Pro
        35              40                  45

cat cgc ggg gca ccg ttg tcc ctg ggt ttc gtt cgc gac ggt aag ctg    192
His Arg Gly Ala Pro Leu Ser Leu Gly Phe Val Arg Asp Gly Lys Leu
    50              55                  60

att tgc ggc tac cac ggt ttg gaa atg ggc tgc gag ggc aaa acg ctc    240
Ile Cys Gly Tyr His Gly Leu Glu Met Gly Cys Glu Gly Lys Thr Leu
65              70                  75                  80

gcg atg ccc ggg cag cgc gtt caa ggc ttc cct tgc atc aaa agc tac    288
Ala Met Pro Gly Gln Arg Val Gln Gly Phe Pro Cys Ile Lys Ser Tyr
                85                  90                  95

gcg gta gaa gag cga tac ggc ttt atc tgg gta tgg cct ggt gat cgc    336
Ala Val Glu Glu Arg Tyr Gly Phe Ile Trp Val Trp Pro Gly Asp Arg
            100                 105                 110

gag ctg gcg gat ccg gcg ctt att cac cac ctg gag tgg gcc gat aat    384
Glu Leu Ala Asp Pro Ala Leu Ile His His Leu Glu Trp Ala Asp Asn
        115                 120                 125

ccg gag tgg gcc tat ggt ggc ggt ctc tac cac atc gct tgt gat tac    432
Pro Glu Trp Ala Tyr Gly Gly Gly Leu Tyr His Ile Ala Cys Asp Tyr
    130                 135                 140

cgc ctg atg atc gac aac ctc atg gat ctc acc cat gag acc tat gtg    480
Arg Leu Met Ile Asp Asn Leu Met Asp Leu Thr His Glu Thr Tyr Val
145                 150                 155                 160

cat gcc tcc agc atc ggt caa aag gaa att gac gag gca ccg gtc agt    528
His Ala Ser Ser Ile Gly Gln Lys Glu Ile Asp Glu Ala Pro Val Ser
                165                 170                 175

act cgt gtc gag ggc gac acc gtg att acc agc cgg tac atg gat aac    576
Thr Arg Val Glu Gly Asp Thr Val Ile Thr Ser Arg Tyr Met Asp Asn
            180                 185                 190

gtc atg gcc cct ccg ttc tgg cgt gct gcg ctt cgt ggc aac ggc ttg    624
Val Met Ala Pro Pro Phe Trp Arg Ala Ala Leu Arg Gly Asn Gly Leu
        195                 200                 205

gcc gac gat gta ccg gtt gat cgc tgg cag atc tgc cga ttc gct cct    672
Ala Asp Asp Val Pro Val Asp Arg Trp Gln Ile Cys Arg Phe Ala Pro
    210                 215                 220

ccg agt cac gta ctg atc gaa gta ggt gtg gct cat gcg ggc aaa ggc    720
Pro Ser His Val Leu Ile Glu Val Gly Val Ala His Ala Gly Lys Gly
225                 230                 235                 240

gga tat gac gcg ccg gcg gaa tac aag gcc ggc agc ata gtg gtc gac    768
Gly Tyr Asp Ala Pro Ala Glu Tyr Lys Ala Gly Ser Ile Val Val Asp
            245                 250                 255
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ttc atc acg ccg gag agt gat acc tcg att tgg tac ttc tgg ggc atg    816
Phe Ile Thr Pro Glu Ser Asp Thr Ser Ile Trp Tyr Phe Trp Gly Met
        260                 265                 270

gct cgc aac ttc cgt ccg cag ggc acg gag ctg act gaa acc att cgt    864
Ala Arg Asn Phe Arg Pro Gln Gly Thr Glu Leu Thr Glu Thr Ile Arg
        275                 280                 285

gtt ggt cag ggc aag att ttt gcc gag gac ctg gac atg ctg gag cag    912
Val Gly Gln Gly Lys Ile Phe Ala Glu Asp Leu Asp Met Leu Glu Gln
    290                 295                 300

cag cag cgc aat ctg ctg gcc tac ccg gag cgc cag ttg ctc aag ctg    960
Gln Gln Arg Asn Leu Leu Ala Tyr Pro Glu Arg Gln Leu Leu Lys Leu
305                 310                 315                 320

aat atc gat gcc ggc ggg gtt cag tca cgg cgc gtc att gat cgg att    1008
Asn Ile Asp Ala Gly Gly Val Gln Ser Arg Arg Val Ile Asp Arg Ile
                325                 330                 335

ctc gca gct gaa caa gag gcc gca gac gca gcg ctg atc gcg aga agt    1056
Leu Ala Ala Glu Gln Glu Ala Ala Asp Ala Ala Leu Ile Ala Arg Ser
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gca tca tga                                                        1065
Ala Ser


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<212> PRT
<213> Pseudomonas sp.

<400> 4
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            20                  25                  30

Tyr Arg Gly Pro Glu Gly Arg Val Ala Ala Val Glu Asp Phe Cys Pro
            35                  40                  45

His Arg Gly Ala Pro Leu Ser Leu Gly Phe Val Arg Asp Gly Lys Leu
        50                  55                  60

Ile Cys Gly Tyr His Gly Leu Glu Met Gly Cys Glu Gly Lys Thr Leu
65                  70                  75                  80

Ala Met Pro Gly Gln Arg Val Gln Gly Phe Pro Cys Ile Lys Ser Tyr
                85                  90                  95

Ala Val Glu Glu Arg Tyr Gly Phe Ile Trp Val Trp Pro Gly Asp Arg
            100                 105                 110
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Glu Leu Ala Asp Pro Ala Leu Ile His His Leu Glu Trp Ala Asp Asn
        115                 120                 125

Pro Glu Trp Ala Tyr Gly Gly Gly Leu Tyr His Ile Ala Cys Asp Tyr
        130                 135                 140

Arg Leu Met Ile Asp Asn Leu Met Asp Leu Thr His Glu Thr Tyr Val
145                 150                 155                 160

His Ala Ser Ser Ile Gly Gln Lys Glu Ile Asp Glu Ala Pro Val Ser
                165                 170                 175

Thr Arg Val Glu Gly Asp Thr Val Ile Thr Ser Arg Tyr Met Asp Asn
                180                 185                 190

Val Met Ala Pro Pro Phe Trp Arg Ala Ala Leu Arg Gly Asn Gly Leu
                195                 200                 205

Ala Asp Asp Val Pro Val Asp Arg Trp Gln Ile Cys Arg Phe Ala Pro
        210                 215                 220

Pro Ser His Val Leu Ile Glu Val Gly Val Ala His Ala Gly Lys Gly
225                 230                 235                 240

Gly Tyr Asp Ala Pro Ala Glu Tyr Lys Ala Gly Ser Ile Val Val Asp
                245                 250                 255

Phe Ile Thr Pro Glu Ser Asp Thr Ser Ile Trp Tyr Phe Trp Gly Met
                260                 265                 270

Ala Arg Asn Phe Arg Pro Gln Gly Thr Glu Leu Thr Glu Thr Ile Arg
        275                 280                 285

Val Gly Gln Gly Lys Ile Phe Ala Glu Asp Leu Asp Met Leu Glu Gln
        290                 295                 300

Gln Gln Arg Asn Leu Leu Ala Tyr Pro Glu Arg Gln Leu Leu Lys Leu
305                 310                 315                 320

Asn Ile Asp Ala Gly Gly Val Gln Ser Arg Arg Val Ile Asp Arg Ile
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Leu Ala Ala Glu Gln Glu Ala Ala Asp Ala Ala Leu Ile Ala Arg Ser
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Ala Ser


<210> 5
<211> 954
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
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<222> (1)..(951)
<223> product = "Vanillin-O-Demethylase"/ gene = "vanB"

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  1               5                  10                  15

att agc ctt gag ttt gtc cgg gct gac ggt ggc ttg ctt ccg cct gtc      96
Ile Ser Leu Glu Phe Val Arg Ala Asp Gly Gly Leu Leu Pro Pro Val
             20                  25                  30

gag gcc ggc gcc cac gtc gat gtg cat ctt cct ggc ggc ctg att cgg     144
Glu Ala Gly Ala His Val Asp Val His Leu Pro Gly Gly Leu Ile Arg
         35                  40                  45

cag tac tcg ctc tgg aat caa cca ggg gcg cag agc cat tac tgc atc     192
Gln Tyr Ser Leu Trp Asn Gln Pro Gly Ala Gln Ser His Tyr Cys Ile
     50                  55                  60

ggt gtt ctg aag gac ccg gcg tct cgt ggt ggt tcg aag gcg gtg cac     240
Gly Val Leu Lys Asp Pro Ala Ser Arg Gly Gly Ser Lys Ala Val His
 65                  70                  75                  80

gag aat ctt cgc gtc ggg atg cgc gtg caa att agc gag ccg agg aac     288
Glu Asn Leu Arg Val Gly Met Arg Val Gln Ile Ser Glu Pro Arg Asn
                 85                  90                  95

cta ttc cca ttg gaa gag ggg gtg gag cgg agt ctg ctg ttc gcg ggc     336
Leu Phe Pro Leu Glu Glu Gly Val Glu Arg Ser Leu Leu Phe Ala Gly
             100                 105                 110

ggg att ggc att acg ccg att ctg tgt atg gct caa gaa tta gca gca     384
Gly Ile Gly Ile Thr Pro Ile Leu Cys Met Ala Gln Glu Leu Ala Ala
         115                 120                 125

cgc gag caa gat ttc gag ttg cat tat tgc gcg cgt tcg acc gac cga     432
Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg
     130                 135                 140

gcg gcg ttc gtt gaa tgg ctt aag gtt tgc gac ttt gct gat cac gta     480
Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val
145                 150                 155                 160

cgt ttc cac ttt gac aat ggc ccg gat cag caa aaa ctg aat gcc gca     528
Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala
                 165                 170                 175

gcg ctg cta gcg gcc gag gcc gaa ggt acc cac ctt tat gtc tgt ggg     576
Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly
             180                 185                 190

ccc ggc ggg ttc atg ggg cat gtg ctt gat acc gcg aag gag cag ggc     624
Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly
         195                 200                 205

tgg gct gac aat cga ctg cat cga gag tat ttc gcc gcg gcg ccg aat     672
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Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn
    210                 215             220

gtg agt gct gac gat ggc agt ttc gag gtg cgg att cac agc acc gga   720
Val Ser Ala Asp Asp Gly Ser Phe Glu Val Arg Ile His Ser Thr Gly
225                 230                 235                 240

caa gtg ctt cag gtc ccc gcg gat caa acg gtc tcc cag gtg ctc gat   768
Gln Val Leu Gln Val Pro Ala Asp Gln Thr Val Ser Gln Val Leu Asp
                245                 250                 255

gcg gcc gga att atc gtt ccc gtt tct tgt gag cag ggc atc tgc ggt   816
Ala Ala Gly Ile Ile Val Pro Val Ser Cys Glu Gln Gly Ile Cys Gly
                260                 265                 270

act tgc atc act cgg gtg gta gac gga gag cct gat cat cgt gac ttc   864
Thr Cys Ile Thr Arg Val Val Asp Gly Glu Pro Asp His Arg Asp Phe
        275                 280                 285

ttc ctc acg gat gcg gag aag gca aag aac gac cag ttc acc ccc tgt   912
Phe Leu Thr Asp Ala Glu Lys Ala Lys Asn Asp Gln Phe Thr Pro Cys
        290                 295                 300

tgc tcg cga gcc aag agc gcc tgt ttg gtc ttg gat ctc taa           954
Cys Ser Arg Ala Lys Ser Ala Cys Leu Val Leu Asp Leu
305                 310                 315


<210> 6
<211> 317
<212> PRT
<213> Pseudomonas sp.

<400> 6
Met Ile Glu Val Ile Ile Ser Ala Met Arg Leu Val Ala Gln Asp Ile
  1               5               10                  15

Ile Ser Leu Glu Phe Val Arg Ala Asp Gly Gly Leu Leu Pro Pro Val
            20              25                  30

Glu Ala Gly Ala His Val Asp Val His Leu Pro Gly Gly Leu Ile Arg
            35                  40                  45

Gln Tyr Ser Leu Trp Asn Gln Pro Gly Ala Gln Ser His Tyr Cys Ile
    50                  55                  60

Gly Val Leu Lys Asp Pro Ala Ser Arg Gly Gly Ser Lys Ala Val His
65                  70                  75                  80

Glu Asn Leu Arg Val Gly Met Arg Val Gln Ile Ser Glu Pro Arg Asn
                85                  90                  95

Leu Phe Pro Leu Glu Glu Gly Val Glu Arg Ser Leu Leu Phe Ala Gly
            100                 105                 110

Gly Ile Gly Ile Thr Pro Ile Leu Cys Met Ala Gln Glu Leu Ala Ala
        115                 120                 125
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Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg
    130             135             140
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Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val
145             150             155             160
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Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala
            165             170             175
```

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Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly
            180             185             190
```

```
Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly
        195             200             205
```

```
Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn
    210             215             220
```

```
Val Ser Ala Asp Asp Gly Ser Phe Glu Val Arg Ile His Ser Thr Gly
225             230             235             240
```

```
Gln Val Leu Gln Val Pro Ala Asp Gln Thr Val Ser Gln Val Leu Asp
            245             250             255
```

```
Ala Ala Gly Ile Ile Val Pro Val Ser Cys Glu Gln Gly Ile Cys Gly
            260             265             270
```

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Thr Cys Ile Thr Arg Val Val Asp Gly Glu Pro Asp His Arg Asp Phe
            275             280             285
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Phe Leu Thr Asp Ala Glu Lys Ala Lys Asn Asp Gln Phe Thr Pro Cys
    290             295             300
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Cys Ser Arg Ala Lys Ser Ala Cys Leu Val Leu Asp Leu
305             310             315
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<210> 7
<211> 1119
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1116)
<223> product = "Formaldehyd-Dehydrogenase"/ gene =
      "fdh"

<400> 7
atg atc aaa tcc cgc gcc gct gtg gcg ttc gca ccc aat cag cca ttg    48
Met Ile Lys Ser Arg Ala Ala Val Ala Phe Ala Pro Asn Gln Pro Leu
  1               5              10              15
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cag atc gtc gaa gtg gac gtg gct ccg ccc aag gcc ggt gaa gtc ctg    96
Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu
            20                  25                  30

gtg cgg gtc gtg gcc acc ggc gtt tgc cac acc gat gcc tac acc ctg   144
Val Arg Val Val Ala Thr Gly Val Cys His Thr Asp Ala Tyr Thr Leu
            35                  40                  45

tcc ggc gct gat tcc gag ggc gtt ttc ccc tgc atc ctt ggt cac gaa   192
Ser Gly Ala Asp Ser Glu Gly Val Phe Pro Cys Ile Leu Gly His Glu
    50                  55                  60

ggc ggc ggc att gtc gaa gcg gtg ggc gag ggc gtc acc tcg ctg gcg   240
Gly Gly Gly Ile Val Glu Ala Val Gly Glu Gly Val Thr Ser Leu Ala
65                  70                  75                  80

gtc ggc gac cac gtg atc ccg ctc tac acg gcc gaa tgc cgt gag tgc   288
Val Gly Asp His Val Ile Pro Leu Tyr Thr Ala Glu Cys Arg Glu Cys
                85                  90                  95

aag ttc ttc aag tcc ggc aag acc aac ctg tgc cag aaa gtg cgt gct   336
Lys Phe Phe Lys Ser Gly Lys Thr Asn Leu Cys Gln Lys Val Arg Ala
                100                 105                 110

act cag ggc aag ggt ctg atg ccg gac ggc acc tcc cgc ttc agc tac   384
Thr Gln Gly Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Ser Tyr
        115                 120                 125

aac ggt cag ccg atc tac cac tac atg ggc tgc tcg acc ttc tcc gag   432
Asn Gly Gln Pro Ile Tyr His Tyr Met Gly Cys Ser Thr Phe Ser Glu
        130                 135                 140

tac acc gtg ctg ccg gaa atc tcc ctg gcg aag att ccc aag aat gcg   480
Tyr Thr Val Leu Pro Glu Ile Ser Leu Ala Lys Ile Pro Lys Asn Ala
145                 150                 155                 160

ccg ctg gag aaa gtc tgc ctg ctg ggc tgc ggc gtg acc acc ggc att   528
Pro Leu Glu Lys Val Cys Leu Leu Gly Cys Gly Val Thr Thr Gly Ile
                165                 170                 175

ggc gcg gtg ctg aac act gcc aag gtg gag gag ggt gct acc gtg gcc   576
Gly Ala Val Leu Asn Thr Ala Lys Val Glu Glu Gly Ala Thr Val Ala
                180                 185                 190

atc ttc ggc ctg ggc ggc atc ggc ttg gcg gcg atc atc ggc gcg aag   624
Ile Phe Gly Leu Gly Gly Ile Gly Leu Ala Ala Ile Ile Gly Ala Lys
        195                 200                 205

atg gcc aag gcc tcg cgc atc atc gcc atc gac atc aat ccg tcc aag   672
Met Ala Lys Ala Ser Arg Ile Ile Ala Ile Asp Ile Asn Pro Ser Lys
210                 215                 220

ttc gat gtg gct cgc gag ctg ggc gcc act gac ttc gtc aat ccg aac   720
Phe Asp Val Ala Arg Glu Leu Gly Ala Thr Asp Phe Val Asn Pro Asn
225                 230                 235                 240

gat cac gcg aag ccg atc cag gat gtc atc gtc gag atg act gat ggc   768
```

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Asp His Ala Lys Pro Ile Gln Asp Val Ile Val Glu Met Thr Asp Gly
            245             250             255

ggt gtg gac tac agc ttc gag tgc atc ggc aac gtt cga ctc atg cgc    816
Gly Val Asp Tyr Ser Phe Glu Cys Ile Gly Asn Val Arg Leu Met Arg
            260             265             270

gca gca ctc gag tgc tgc cac aag ggc tgg ggc gaa tcc gtg atc atc    864
Ala Ala Leu Glu Cys Cys His Lys Gly Trp Gly Glu Ser Val Ile Ile
        275             280             285

ggc gtg gcg ccg gcg ggg gcc gaa atc aac acc cgt ccg ttc cac ctg    912
Gly Val Ala Pro Ala Gly Ala Glu Ile Asn Thr Arg Pro Phe His Leu
        290             295             300

gtg acc ggt cgc gtc tgg cgg ggt tcg gcg ttc ggt ggc gta aag ggc    960
Val Thr Gly Arg Val Trp Arg Gly Ser Ala Phe Gly Gly Val Lys Gly
305             310             315             320

cgc acc gaa ctg ccg agc tac gtg gag aag gca cag cag ggc gag atc   1008
Arg Thr Glu Leu Pro Ser Tyr Val Glu Lys Ala Gln Gln Gly Glu Ile
            325             330             335

ccg ctg gac acc ttc atc act cac acc atg ggc ctg gac gac atc aac   1056
Pro Leu Asp Thr Phe Ile Thr His Thr Met Gly Leu Asp Asp Ile Asn
            340             345             350

acg gcc ttc gac ctg atg gac gaa ggg aag agc atc cgc tct gtt gtt   1104
Thr Ala Phe Asp Leu Met Asp Glu Gly Lys Ser Ile Arg Ser Val Val
            355             360             365

caa ttg agt cgc tag                                                1119
Gln Leu Ser Arg
        370


<210> 8
<211> 372
<212> PRT
<213> Pseudomonas sp.

<400> 8
Met Ile Lys Ser Arg Ala Ala Val Ala Phe Ala Pro Asn Gln Pro Leu
 1               5              10              15

Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu
            20              25              30

Val Arg Val Val Ala Thr Gly Val Cys His Thr Asp Ala Tyr Thr Leu
        35              40              45

Ser Gly Ala Asp Ser Glu Gly Val Phe Pro Cys Ile Leu Gly His Glu
    50              55              60

Gly Gly Gly Ile Val Glu Ala Val Gly Glu Gly Val Thr Ser Leu Ala
 65              70              75              80
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Val Gly Asp His Val Ile Pro Leu Tyr Thr Ala Glu Cys Arg Glu Cys
            85              90                  95

Lys Phe Phe Lys Ser Gly Lys Thr Asn Leu Cys Gln Lys Val Arg Ala
        100             105             110

Thr Gln Gly Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Ser Tyr
        115             120             125

Asn Gly Gln Pro Ile Tyr His Tyr Met Gly Cys Ser Thr Phe Ser Glu
    130             135             140

Tyr Thr Val Leu Pro Glu Ile Ser Leu Ala Lys Ile Pro Lys Asn Ala
145             150             155             160

Pro Leu Glu Lys Val Cys Leu Leu Gly Cys Gly Val Thr Thr Gly Ile
            165             170             175

Gly Ala Val Leu Asn Thr Ala Lys Val Glu Glu Gly Ala Thr Val Ala
        180             185             190

Ile Phe Gly Leu Gly Gly Ile Gly Leu Ala Ala Ile Ile Gly Ala Lys
        195             200             205

Met Ala Lys Ala Ser Arg Ile Ile Ala Ile Asp Ile Asn Pro Ser Lys
    210             215             220

Phe Asp Val Ala Arg Glu Leu Gly Ala Thr Asp Phe Val Asn Pro Asn
225             230             235             240

Asp His Ala Lys Pro Ile Gln Asp Val Ile Val Glu Met Thr Asp Gly
            245             250             255

Gly Val Asp Tyr Ser Phe Glu Cys Ile Gly Asn Val Arg Leu Met Arg
            260             265             270

Ala Ala Leu Glu Cys Cys His Lys Gly Trp Gly Glu Ser Val Ile Ile
        275             280             285

Gly Val Ala Pro Ala Gly Ala Glu Ile Asn Thr Arg Pro Phe His Leu
    290             295             300

Val Thr Gly Arg Val Trp Arg Gly Ser Ala Phe Gly Gly Val Lys Gly
305             310             315             320

Arg Thr Glu Leu Pro Ser Tyr Val Glu Lys Ala Gln Gln Gly Glu Ile
            325             330             335

Pro Leu Asp Thr Phe Ile Thr His Thr Met Gly Leu Asp Asp Ile Asn
            340             345             350

Thr Ala Phe Asp Leu Met Asp Glu Gly Lys Ser Ile Arg Ser Val Val
        355             360             365

Gln Leu Ser Arg
    370
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<210> 9
<211> 1638
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1635)
<223> product = "gamma-Glutamylcystein-Synthetase" /
        gene = "gcs"

<400> 9
atg ccg caa act ctt gct gga cgg ttg agt ctg tta tcc ggc acc gac   48
Met Pro Gln Thr Leu Ala Gly Arg Leu Ser Leu Leu Ser Gly Thr Asp
 1   5   10   15

gaa tta acc ctg ctt ctt cgg ggt ggt cgg ggc att gag cgt gaa gcc   96
Glu Leu Thr Leu Leu Leu Arg Gly Gly Arg Gly Ile Glu Arg Glu Ala
                20   25   30

ttg cgg gtc gat gtt caa ggt gaa ctg gcg ctg acg cct cac ccg gcg   144
Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala
            35   40   45

gcg ctt ggc tct gcg ttg acc cat ccg aca att act acg gat tac gcc   192
Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala
        50   55   60

gag gcc ctg ctt gag ttg atc act cgg ccg gca acc gat tgt gcg caa   240
Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln
 65   70   75   80

gcc ttg gct gag ctg gag gag ctt cac cgt ttc gtt cat tcg aga ctt   288
Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu
                85   90   95

gag ggg gag tat ctc tgg aat ctg tcc atg cct ggc aga ttg ccg gtt   336
Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val
                100   105   110

gat gag caa atc ccg att gct tgg tat gga cca tca aat cca ggc atg   384
Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met
            115   120   125

ttg cgc cac gtt tat cgc cgt ggc cta gct ctg cgt tat ggc aag cga   432
Leu Arg His Val Tyr Arg Arg Gly Leu Ala Leu Arg Tyr Gly Lys Arg
        130   135   140

atg caa tgc atc gca ggg att cac tac aac tac tca ctg ccg cca gag   480
Met Gln Cys Ile Ala Gly Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu
145   150   155   160

ctt ttc gct gtc ctg acc aag gca gag gtc ggg tct ccc aag tta ctg   528

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Leu Phe Ala Val Leu Thr Lys Ala Glu Val Gly Ser Pro Lys Leu Leu
                165                 170             175


gag cgc cag tca gca gct tac atg cgc caa att cgc aac ctt cgg caa    576
Glu Arg Gln Ser Ala Ala Tyr Met Arg Gln Ile Arg Asn Leu Arg Gln
            180                 185             190

tac ggt tgg ttg ctg gcc tac ttg ttc ggc gct tcc ccc gcc atc tgc    624
Tyr Gly Trp Leu Leu Ala Tyr Leu Phe Gly Ala Ser Pro Ala Ile Cys
            195                 200             205

aag agc ttc ttg ggg ggc gag aga gat gag cta gct cgc atg ggg ggc    672
Lys Ser Phe Leu Gly Gly Glu Arg Asp Glu Leu Ala Arg Met Gly Gly
            210                 215             220

gat acg ctt tac atg ccc tat gca acc agc ttg cgc atg agt gac atc    720
Asp Thr Leu Tyr Met Pro Tyr Ala Thr Ser Leu Arg Met Ser Asp Ile
225                 230             235                 240

ggg tac cgc aac cgt gcc atg gat gat cta tct ccc agc ctg aat gat    768
Gly Tyr Arg Asn Arg Ala Met Asp Asp Leu Ser Pro Ser Leu Asn Asp
            245                 250             255

ctg ggt gcc tat att cgc gat att tgc cgt gct ctt cac act ccc gat    816
Leu Gly Ala Tyr Ile Arg Asp Ile Cys Arg Ala Leu His Thr Pro Asp
            260                 265             270

gcc cag tac cag gcg ctg ggt gtg ttt gca cag ggc gag tgg cgg cag    864
Ala Gln Tyr Gln Ala Leu Gly Val Phe Ala Gln Gly Glu Trp Arg Gln
            275                 280             285

tta aac gcc aat cta ttg cag ttg gat agt gag tac tac gca ctg gcg    912
Leu Asn Ala Asn Leu Leu Gln Leu Asp Ser Glu Tyr Tyr Ala Leu Ala
            290                 295             300

cga ccg aag tca gcg ccc gag cgg ggg gag cga aac ctg gat gct ctc    960
Arg Pro Lys Ser Ala Pro Glu Arg Gly Glu Arg Asn Leu Asp Ala Leu
305                 310             315                 320

gct agg cgt gga gtc cag tat gtg gag ctg cgc gca ctg gat ctc gat   1008
Ala Arg Arg Gly Val Gln Tyr Val Glu Leu Arg Ala Leu Asp Leu Asp
            325                 330             335

cca ttc tcc ccg tta ggc att ggc ctg acc tgc gcc aag ttc ctc gat   1056
Pro Phe Ser Pro Leu Gly Ile Gly Leu Thr Cys Ala Lys Phe Leu Asp
            340                 345             350

ggc ttt ttg ctt ttc tgc ttg ttg tct gag gcg ccg gtt gat gat cga   1104
Gly Phe Leu Leu Phe Cys Leu Leu Ser Glu Ala Pro Val Asp Asp Arg
            355                 360             365

aat gcc cag cgt tca aga ccg gga aaa tct gag cct ggc cgg caa gta   1152
Asn Ala Gln Arg Ser Arg Pro Gly Lys Ser Glu Pro Gly Arg Gln Val
370                 375             380
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cgg gcg tca cct ggc tta aag ctg cat cgg aat ggt cag tcc att ctc    1200
Arg Ala Ser Pro Gly Leu Lys Leu His Arg Asn Gly Gln Ser Ile Leu
385                 390                 395                 400


ctc aag gat tgg gcg cag gaa gtg ttg acg gag gtt cag gcc tgt gtg    1248
Leu Lys Asp Trp Ala Gln Glu Val Leu Thr Glu Val Gln Ala Cys Val
                405                 410                 415

gaa ttg ctc gac agt gca aat ggg ggc tca tct cac gca ttg gct tgg    1296
Glu Leu Leu Asp Ser Ala Asn Gly Gly Ser Ser His Ala Leu Ala Trp
            420                 425                 430

tca gca cag gag gaa aag gtg ctt aat ccg gat tgt gcg cca tca gct    1344
Ser Ala Gln Glu Glu Lys Val Leu Asn Pro Asp Cys Ala Pro Ser Ala
        435                 440                 445

cag gtg ctc gca gag ata cac aga cac ggt ggg agc ttc acg gca ttt    1392
Gln Val Leu Ala Glu Ile His Arg His Gly Gly Ser Phe Thr Ala Phe
    450                 455                 460

ggt cgc caa tta gct atc gac cat gca aaa cac ttc agt gcc tcc tcg    1440
Gly Arg Gln Leu Ala Ile Asp His Ala Lys His Phe Ser Ala Ser Ser
465                 470                 475                 480

ctt gag gct ggc gta gcc aaa gcg ctt gac ctc cag gcg acg tcg tct    1488
Leu Glu Ala Gly Val Ala Lys Ala Leu Asp Leu Gln Ala Thr Ser Ser
                485                 490                 495

ctg cgc gag cag cat caa ttg gag gcc aac gac cgt gcg cca ttt tct    1536
Leu Arg Glu Gln His Gln Leu Glu Ala Asn Asp Arg Ala Pro Phe Ser
            500                 505                 510

gac tac ctt cag caa ttc tcc ctg gct ttc ggt caa tcc gtc ggc gcc    1584
Asp Tyr Leu Gln Gln Phe Ser Leu Ala Phe Gly Gln Ser Val Gly Ala
        515                 520                 525

tct cgt gcg ccc aac cct acc gcg cac ctc atc gat ctg acc cct cct    1632
Ser Arg Ala Pro Asn Pro Thr Ala His Leu Ile Asp Leu Thr Pro Pro
    530                 535                 540

gtc taa                                                            1638
Val
545



<210> 10
<211> 545
<212> PRT
<213> Pseudomonas sp.

<400> 10
Met Pro Gln Thr Leu Ala Gly Arg Leu Ser Leu Leu Ser Gly Thr Asp
    1               5                   10                  15


Glu Leu Thr Leu Leu Leu Arg Gly Gly Arg Gly Ile Glu Arg Glu Ala
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                  20                      25                      30

       Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala
               35                  40                  45



       Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala
               50                  55                  60

       Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln
       65                  70                  75                  80

       Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu
                       85                  90                  95

       Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val
                       100                 105                 110

       Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met
                   115                 120                 125

       Leu Arg His Val Tyr Arg Arg Gly Leu Ala Leu Arg Tyr Gly Lys Arg
           130                 135                 140

       Met Gln Cys Ile Ala Gly Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu
       145                 150                 155                 160

       Leu Phe Ala Val Leu Thr Lys Ala Glu Val Gly Ser Pro Lys Leu Leu
                       165                 170                 175

       Glu Arg Gln Ser Ala Ala Tyr Met Arg Gln Ile Arg Asn Leu Arg Gln
                   180                 185                 190

       Tyr Gly Trp Leu Leu Ala Tyr Leu Phe Gly Ala Ser Pro Ala Ile Cys
                   195                 200                 205

       Lys Ser Phe Leu Gly Gly Glu Arg Asp Glu Leu Ala Arg Met Gly Gly
           210                 215                 220

       Asp Thr Leu Tyr Met Pro Tyr Ala Thr Ser Leu Arg Met Ser Asp Ile
       225                 230                 235                 240

       Gly Tyr Arg Asn Arg Ala Met Asp Asp Leu Ser Pro Ser Leu Asn Asp
                   245                 250                 255

       Leu Gly Ala Tyr Ile Arg Asp Ile Cys Arg Ala Leu His Thr Pro Asp
                   260                 265                 270

       Ala Gln Tyr Gln Ala Leu Gly Val Phe Ala Gln Gly Glu Trp Arg Gln
                   275                 280                 285

       Leu Asn Ala Asn Leu Leu Gln Leu Asp Ser Glu Tyr Tyr Ala Leu Ala
           290                 295                 300

       Arg Pro Lys Ser Ala Pro Glu Arg Gly Glu Arg Asn Leu Asp Ala Leu
       305                 310                 315                 320
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Ala Arg Arg Gly Val Gln Tyr Val Glu Leu Arg Ala Leu Asp Leu Asp
                325   330   335

Pro Phe Ser Pro Leu Gly Ile Gly Leu Thr Cys Ala Lys Phe Leu Asp
                340   345   350

Gly Phe Leu Leu Phe Cys Leu Leu Ser Glu Ala Pro Val Asp Asp Arg
                355   360   365

Asn Ala Gln Arg Ser Arg Pro Gly Lys Ser Glu Pro Gly Arg Gln Val
        370   375   380

Arg Ala Ser Pro Gly Leu Lys Leu His Arg Asn Gly Gln Ser Ile Leu
385   390   395   400

Leu Lys Asp Trp Ala Gln Glu Val Leu Thr Glu Val Gln Ala Cys Val
                405   410   415

Glu Leu Leu Asp Ser Ala Asn Gly Gly Ser Ser His Ala Leu Ala Trp
                420   425   430

Ser Ala Gln Glu Glu Lys Val Leu Asn Pro Asp Cys Ala Pro Ser Ala
                435   440   445

Gln Val Leu Ala Glu Ile His Arg His Gly Gly Ser Phe Thr Ala Phe
        450   455   460

Gly Arg Gln Leu Ala Ile Asp His Ala Lys His Phe Ser Ala Ser Ser
465   470   475   480

Leu Glu Ala Gly Val Ala Lys Ala Leu Asp Leu Gln Ala Thr Ser Ser
                485   490   495

Leu Arg Glu Gln His Gln Leu Glu Ala Asn Asp Arg Ala Pro Phe Ser
                500   505   510

Asp Tyr Leu Gln Gln Phe Ser Leu Ala Phe Gly Gln Ser Val Gly Ala
        515   520   525

Ser Arg Ala Pro Asn Pro Thr Ala His Leu Ile Asp Leu Thr Pro Pro
        530   535   540

Val
545

<210> 11
<211> 354
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(351)
<223> product = "Cytochrom C UE-Eugenol-Hydroxylase" /

gene = "chyA"

<400> 11
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atg atg aat gtt aat tat aag gct gtc ggg gcg agc cta ctc ctc gcc    48
Met Met Asn Val Asn Tyr Lys Ala Val Gly Ala Ser Leu Leu Leu Ala
  1               5                  10                  15

ttc atc tct cag gga gct tgg gca gag agc ccc gca gcc tct ggc aat    96
Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn
              20                  25                  30

acc cct gac att tat cga aag acc tgc acc tac tgc cat gag cct act   144
Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr
          35                  40                  45

gtc aac aat ggc cgg gtc att gcc cga agc ctc ggg ccg act ctg cga   192
Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg
      50                  55                  60

ggg cgc cag atc cct cca cag tac acg gag tac atg gtg cgt cat gga   240
Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly
 65                  70                  75                  80

cgc ggg gca atg cct gca ttc tct gaa gca gaa gtg cct ccg gcg gag   288
Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu
                  85                  90                  95

ctg aaa gtt ctg ggc gat tgg att cag caa agc agt gct ccc aaa gac   336
Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp
                 100                 105                 110

gct gga gtc gcg cca tga                                           354
Ala Gly Val Ala Pro
                 115
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<210> 12
<211> 117
<212> PRT
<213> Pseudomonas sp.

<400> 12
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Met Met Asn Val Asn Tyr Lys Ala Val Gly Ala Ser Leu Leu Leu Ala
  1               5                  10                  15

Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn
              20                  25                  30

Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr
          35                  40                  45

Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg
      50                  55                  60

Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly
 65                  70                  75                  80
```

Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu
              85   90   95

Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp
              100   105   110

Ala Gly Val Ala Pro
         115

<210> 13
<211> 687
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(684)
<223> gene = "ORF5"

<400> 13
atg act acc cgt cgc aac ttt cta ata ggc gcg tcg cag gtg ggg gca   48
Met Thr Thr Arg Arg Asn Phe Leu Ile Gly Ala Ser Gln Val Gly Ala
  1   5   10   15

ttg gtg atg atg tcg ccg aaa ttg gtc ttc cgt acg ccg ctc aag cag   96
Leu Val Met Met Ser Pro Lys Leu Val Phe Arg Thr Pro Leu Lys Gln
            20   25   30

aag ccc gtg cgc atc ctg tcg acc ggg ctg gcc ggt gag caa gag ttt   144
Lys Pro Val Arg Ile Leu Ser Thr Gly Leu Ala Gly Glu Gln Glu Phe
        35   40   45

cac tcg atg ctt cgc gcg cga ttg acc cat acg ggt cag gtc gac atc   192
His Ser Met Leu Arg Ala Arg Leu Thr His Thr Gly Gln Val Asp Ile
    50   55   60

gcg tcg gta ccg ctg gac gca gct att tgg gct tct ccc gct cga ctt   240
Ala Ser Val Pro Leu Asp Ala Ala Ile Trp Ala Ser Pro Ala Arg Leu
65   70   75   80

gcc cag gca atg gat gcg ttg aat ggt acg cgt ctg atc gct ttt gtt   288
Ala Gln Ala Met Asp Ala Leu Asn Gly Thr Arg Leu Ile Ala Phe Val
                85   90   95

gag ccc agg aac gaa ttg ata ctg atg caa ttc ttg atg gat cgc ggg   336
Glu Pro Arg Asn Glu Leu Ile Leu Met Gln Phe Leu Met Asp Arg Gly
            100   105   110

gct gcg gtg ctt att caa ggt gag cat gcg gtg gac agc aag ggg gtc   384
Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val
        115   120   125

tct cgg cac gac ttt ctg agt acc cca tcc agt gcg gga att gga ggg   432

```
Ser Arg His Asp Phe Leu Ser Thr Pro Ser Ser Ala Gly Ile Gly Gly
    130                 135             140

gcg cta gcc gac agc ctg gca aaa ggg ggc tcg ccg ttc tct att tcc    480
Ala Leu Ala Asp Ser Leu Ala Lys Gly Gly Ser Pro Phe Ser Ile Ser
145                 150                 155                 160


gtc cga gcg ctt ggc tcg gta act gct cag cca aga agt aat cag agt    528
Val Arg Ala Leu Gly Ser Val Thr Ala Gln Pro Arg Ser Asn Gln Ser
                165                 170                 175

gag gtg gcc acc cac tgg acg acc gct ctg ggg acc tat tat gcc gat    576
Glu Val Ala Thr His Trp Thr Thr Ala Leu Gly Thr Tyr Tyr Ala Asp
                180                 185                 190

atc gca gtg ggg cgc tgg gag ccg cag cgc gaa gtg gcc agc tat gga    624
Ile Ala Val Gly Arg Trp Glu Pro Gln Arg Glu Val Ala Ser Tyr Gly
                195                 200                 205

agt gga cta atc atg gcg gaa cgg ctt gat cgt gtt gcc tca acc ttc    672
Ser Gly Leu Ile Met Ala Glu Arg Leu Asp Arg Val Ala Ser Thr Phe
    210                 215                 220

att gca gat ctc tga                                                 687
Ile Ala Asp Leu
225


<210> 14
<211> 228
<212> PRT
<213> Pseudomonas sp.

<400> 14
Met Thr Thr Arg Arg Asn Phe Leu Ile Gly Ala Ser Gln Val Gly Ala
  1               5                 10                  15

Leu Val Met Met Ser Pro Lys Leu Val Phe Arg Thr Pro Leu Lys Gln
                20              25                  30

Lys Pro Val Arg Ile Leu Ser Thr Gly Leu Ala Gly Glu Gln Glu Phe
            35                  40                  45

His Ser Met Leu Arg Ala Arg Leu Thr His Thr Gly Gln Val Asp Ile
        50                  55                  60

Ala Ser Val Pro Leu Asp Ala Ala Ile Trp Ala Ser Pro Ala Arg Leu
65                  70                  75                  80

Ala Gln Ala Met Asp Ala Leu Asn Gly Thr Arg Leu Ile Ala Phe Val
                85                  90                  95

Glu Pro Arg Asn Glu Leu Ile Leu Met Gln Phe Leu Met Asp Arg Gly
            100                 105                 110
```

```
Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val
        115             120             125

Ser Arg His Asp Phe Leu Ser Thr Pro Ser Ser Ala Gly Ile Gly Gly
        130             135             140

Ala Leu Ala Asp Ser Leu Ala Lys Gly Gly Ser Pro Phe Ser Ile Ser
145             150             155             160

Val Arg Ala Leu Gly Ser Val Thr Ala Gln Pro Arg Ser Asn Gln Ser
            165             170             175

Glu Val Ala Thr His Trp Thr Thr Ala Leu Gly Thr Tyr Tyr Ala Asp
        180             185             190

Ile Ala Val Gly Arg Trp Glu Pro Gln Arg Glu Val Ala Ser Tyr Gly
        195             200             205

Ser Gly Leu Ile Met Ala Glu Arg Leu Asp Arg Val Ala Ser Thr Phe
        210             215             220

Ile Ala Asp Leu
225
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<210> 15
<211> 1554
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1551)
<223> product = " Flavoprotein UE-Eugenol-Hydroxylase" /
      gene = "ehyB"

<400> 15
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atg gaa agc acc gta gtt ctt ccc gag ggt gtc acc ccg gag cag ttc    48
Met Glu Ser Thr Val Val Leu Pro Glu Gly Val Thr Pro Glu Gln Phe
 1               5               10                  15

acc aaa gcc atc agc gag ttc cgt cag gta ttg ggt gag gac agt gtt    96
Thr Lys Ala Ile Ser Glu Phe Arg Gln Val Leu Gly Glu Asp Ser Val
                20              25                  30

ctt gtc act gct gaa cga gtt gtt ccc tat acg aaa ctc ctc att cct   144
Leu Val Thr Ala Glu Arg Val Val Pro Tyr Thr Lys Leu Leu Ile Pro
            35              40                  45

aca cag gat gat gcc cag tac acc ccg gcc ggt gcc ttg act cct tct   192
Thr Gln Asp Asp Ala Gln Tyr Thr Pro Ala Gly Ala Leu Thr Pro Ser
    50              55                  60

tcg gtg gag cag gtc cag aaa gtc atg ggg atc tgc aat aag tac aag   240
Ser Val Glu Gln Val Gln Lys Val Met Gly Ile Cys Asn Lys Tyr Lys
 65              70                  75                  80
```

```
atc ccg gta tgg cca atc tct acc ggt cgg aac tgg ggg tat ggg tcc    288
Ile Pro Val Trp Pro Ile Ser Thr Gly Arg Asn Trp Gly Tyr Gly Ser
                 85                  90                  95

gct tcg cct gca act cct ggg cag atg att ctt gac ctt cgc aag atg    336
Ala Ser Pro Ala Thr Pro Gly Gln Met Ile Leu Asp Leu Arg Lys Met
                100                 105                 110

aac aag atc att gag atc gat gtt gag ggg tgt act gcc ctg ctc gag    384
Asn Lys Ile Ile Glu Ile Asp Val Glu Gly Cys Thr Ala Leu Leu Glu
            115                 120                 125

ccg ggc gtt acc tac cag cag ctt cac gat tac atc aag gag cac aat    432
Pro Gly Val Thr Tyr Gln Gln Leu His Asp Tyr Ile Lys Glu His Asn
        130                 135                 140

ctg ccc ttg atg ctg gat gtg ccg act att ggg cct atg gtt ggc ccg    480
Leu Pro Leu Met Leu Asp Val Pro Thr Ile Gly Pro Met Val Gly Pro
145                 150                 155                 160

gtg ggt aac acg ctg gat cga ggc gtt ggt tat acg ccg tac ggc gag    528
Val Gly Asn Thr Leu Asp Arg Gly Val Gly Tyr Thr Pro Tyr Gly Glu
                165                 170                 175

cac ttc atg atg cag tgt ggt atg gaa gtc gtc atg gcc gat ggc gaa    576
His Phe Met Met Gln Cys Gly Met Glu Val Val Met Ala Asp Gly Glu
                180                 185                 190

atc ctc cgt act ggt atg ggc tcg gtg ccc aaa gcc aag act tgg cag    624
Ile Leu Arg Thr Gly Met Gly Ser Val Pro Lys Ala Lys Thr Trp Gln
            195                 200                 205

gca ttc aaa tgg ggc tat ggt cca tat ctg gac ggt atc ttt acc cag    672
Ala Phe Lys Trp Gly Tyr Gly Pro Tyr Leu Asp Gly Ile Phe Thr Gln
        210                 215                 220

tcc aac ttt ggt gtt gtg aca aag ctc ggg att tgg ttg atg ccc aag    720
Ser Asn Phe Gly Val Val Thr Lys Leu Gly Ile Trp Leu Met Pro Lys
225                 230                 235                 240

ccg cca gtg atc aag tcg ttt atg atc cgt tat ccc aat gaa gct gat    768
Pro Pro Val Ile Lys Ser Phe Met Ile Arg Tyr Pro Asn Glu Ala Asp
                245                 250                 255

gtg gtt aag gca att gat gct ttt cgc ccg ctg cgt att act cag ctg    816
Val Val Lys Ala Ile Asp Ala Phe Arg Pro Leu Arg Ile Thr Gln Leu
                260                 265                 270

att cct aac gtc gtt ttg ttc atg cac ggc atg tac gaa acg gca atc    864
Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile
        275                 280                 285

tgc cgg acg cgt gct gag gtt act tcg gac cca ggt cct att tct gaa    912
Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu
    290                 295                 300
```

```
gcg gac gcc cgc aaa gca ttc aaa gag cta ggc gtt ggc tac tgg aac    960
Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn
305           310               315                   320

gtt tac ttc gcg ctt tac ggc aca gaa gag cag ata gcc gtc aat gaa   1008
Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu
                325               330               335

aag atc gtc cgc ggc atc ctc gaa ccg acg ggg ggt gag atc ctc acc   1056
Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr
                340               345               350

gaa gag gag gct gga gat aac att ctt ttc cat cac cat aag cag ctc   1104
Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu
            355               360               365

atg aac ggc gag atg aca ttg gag gaa atg aat atc tac cag tgg cgc   1152
Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg
        370               375               380

gga gca ggt ggc ggt gct tgc tgg ttt gca ccg gtt gct cag gtc aag   1200
Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys
385                   390               395                   400

ggg cat gag gca gag cag cag gtc aag ctt gct cag aag gtg ctt gca   1248
Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala
                405               410               415

aag cat ggg ttc gat tac acg gcg ggc ttt gcg att ggt tgg cgc gat   1296
Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp
            420               425               430

ctt cac cat gtg atc gat gtg ctg tac gac cgt agc aat gcc gac gag   1344
Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu
        435               440               445

aaa aag cgc gct tac gct tgc ttt gat gaa ttg atc gac gtc ttt gcg   1392
Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala
        450               455               460

gcc gaa ggc ttt gca agt tac agg acc aat att gcc ttt atg gac aaa   1440
Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys
465                   470               475                   480

gtc gcc tct aag ttc ggc gct gag aat aag agg gtc aat cag aag atc   1488
Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile
                485               490               495

aag gct gcc ctt gat cca aac ggc atc atc gct ccc ggc aag tcg ggc   1536
Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly
            500               505               510

att cat ctt ccc aaa taa                                            1554
Ile His Leu Pro Lys
        515
```

<210> 16
<211> 517
<212> PRT
<213> Pseudomonas sp.

<400> 16
Met Glu Ser Thr Val Val Leu Pro Glu Gly Val Thr Pro Glu Gln Phe
 1   5   10   15

Thr Lys Ala Ile Ser Glu Phe Arg Gln Val Leu Gly Glu Asp Ser Val
            20   25   30

Leu Val Thr Ala Glu Arg Val Val Pro Tyr Thr Lys Leu Leu Ile Pro
        35   40   45

Thr Gln Asp Asp Ala Gln Tyr Thr Pro Ala Gly Ala Leu Thr Pro Ser
    50   55   60

Ser Val Glu Gln Val Gln Lys Val Met Gly Ile Cys Asn Lys Tyr Lys
65   70   75   80

Ile Pro Val Trp Pro Ile Ser Thr Gly Arg Asn Trp Gly Tyr Gly Ser
                85   90   95

Ala Ser Pro Ala Thr Pro Gly Gln Met Ile Leu Asp Leu Arg Lys Met
            100   105   110

Asn Lys Ile Ile Glu Ile Asp Val Glu Gly Cys Thr Ala Leu Leu Glu
        115   120   125

Pro Gly Val Thr Tyr Gln Gln Leu His Asp Tyr Ile Lys Glu His Asn
    130   135   140

Leu Pro Leu Met Leu Asp Val Pro Thr Ile Gly Pro Met Val Gly Pro
145   150   155   160

Val Gly Asn Thr Leu Asp Arg Gly Val Gly Tyr Thr Pro Tyr Gly Glu
                165   170   175

His Phe Met Met Gln Cys Gly Met Glu Val Val Met Ala Asp Gly Glu
            180   185   190

Ile Leu Arg Thr Gly Met Gly Ser Val Pro Lys Ala Lys Thr Trp Gln
        195   200   205

Ala Phe Lys Trp Gly Tyr Gly Pro Tyr Leu Asp Gly Ile Phe Thr Gln
    210   215   220

Ser Asn Phe Gly Val Val Thr Lys Leu Gly Ile Trp Leu Met Pro Lys
225   230   235   240

Pro Pro Val Ile Lys Ser Phe Met Ile Arg Tyr Pro Asn Glu Ala Asp
                245   250   255

Val Val Lys Ala Ile Asp Ala Phe Arg Pro Leu Arg Ile Thr Gln Leu

```
                260                     265                     270

Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile
        275                 280                 285

Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu
        290                 295                 300

Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn
305                 310                 315                 320

Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu
                325                 330                 335

Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr
                340                 345                 350

Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu
        355                 360                 365

Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg
        370                 375                 380

Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys
385                 390                 395                 400

Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala
                405                 410                 415

Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp
                420                 425                 430

Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu
        435                 440                 445

Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala
        450                 455                 460

Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys
465                 470                 475                 480

Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile
                485                 490                 495

Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly
                500                 505                 510

Ile His Leu Pro Lys
                515
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<220>
<221> CDS
<222> (1)..(858)
<223> gene = "ORF2"

<400> 17
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atg att gca atc act gcg ggc acc gga agt ctt ggt cgg gct atc gtt      48
Met Ile Ala Ile Thr Ala Gly Thr Gly Ser Leu Gly Arg Ala Ile Val
  1               5                  10                  15

gag cga cta ggg gac tgc ggt ctt atc ggt caa gtt cga ttg acg gct      96
Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala
                 20                  25                  30

cgc gat cct aaa agg ctt cgt gcc gct gcc gag gaa ggg ttt cag gtc     144
Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val
             35                  40                  45

gct aag gcg gat tac gcc gat att ggg agt ctt gac cag gca tta cag     192
Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln
         50                  55                  60

ggg gta gac gta tta ctc ctg att tct ggt act gca ccc aat gaa ata     240
Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile
 65                  70                  75                  80

agg atc caa cag cat aag tcg gtc atc gac gcg gca aaa cga aac ggc     288
Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly
                 85                  90                  95

gtg tcg cgt att gtg tat acc agc ttc ata aat cca agt act cgc agc     336
Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser
             100                 105                 110

agg tct att tgg gcc tcc att cat cgt gaa act gag act tac ctc agg     384
Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg
         115                 120                 125

cag tct ggg gtg aag ttt acg att gtc cga aat aat cag tat gcg tct     432
Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser
     130                 135                 140

aac ctg gat ctg ttg ctg ctg agg gct caa gac agc gga ata ttt gcc     480
Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala
145                 150                 155                 160

att ccc ggg gcg aag ggg cgg gtg gcg tac gtc tct cat cgc gac gtt     528
Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val
                 165                 170                 175

gcc gct gcc atc tgt agt gtc ctg acg acc gcc gga cac gat aac agg     576
Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg
             180                 185                 190

atc tac cag ctc aca ggc tct gag gct ctc aat ggg ctc gag atc gcg     624
Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala
         195                 200                 205
```

```
gag att ctt ggt ggg gtg ctc ggg cgt cca gtg cgc gcg atg gat gcc    672
Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala
    210             215             220

tcg cct gac gag ttt gct gcc agc ttt cgc gag gct gga ttc cct gag    720
Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu
225             230             235             240



ttt atg gtt gaa ggc cta cta agc att tat gcc gct tca ggt gct ggg    768
Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly
            245             250             255

gag tac caa tcc gtc agt cct gat gtt ggg ttg ttg acg gga cga cgt    816
Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg
            260             265             270

gcc gaa tcg atg cga act tac ata cag cgt cta gtt tgg cct tga       861
Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro
            275             280             285


<210> 18
<211> 286
<212> PRT
<213> Pseudomonas sp.

<400> 18
Met Ile Ala Ile Thr Ala Gly Thr Gly Ser Leu Gly Arg Ala Ile Val
  1               5              10                  15

Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala
                20              25                  30

Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val
            35              40                  45

Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln
        50              55                  60

Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile
 65              70              75                  80

Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly
                85              90                  95

Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser
            100             105             110

Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg
            115             120             125

Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser
        130             135             140
```

```
Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala
145             150             155             160

Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val
                165             170             175

Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg
            180             185             190

Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala
        195             200             205

Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala
    210             215             220

Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu
225             230             235             240

Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly
            245             250             255

Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg
            260             265             270

Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro
        275             280             285
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<210> 19
<211> 1011
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1008)
<223> product = "Alkohol-Dehydrogenase" / gene = "adh"

<400> 19
atg aag gct tat gag ctt cac aag att tcg gaa cag gta gag gtc agg     48
Met Lys Ala Tyr Glu Leu His Lys Ile Ser Glu Gln Val Glu Val Arg
  1             5                  10                  15

ctc cag cca act cgg ccc cgc ccg cag ttg aat cat ggc gag gtc ctc     96
Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu
             20                  25                  30

atc agg gtc cat gca gcc tcg ctc aac ttt cgc gat ttg atg atc ttg    144
Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu
            35                  40                  45

gcc ggt cgc tat ccg ggt caa atg aaa ccc gat gtg atc ccg ctg tcc    192
Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser
        50                  55                  60

gat ggt gct ggc gag att gtg gag gtc ggg cct ggc gta tct tcg gag    240
```

```
Asp Gly Ala Gly Glu Ile Val Glu Val Gly Pro Gly Val Ser Ser Glu
 65                  70                  75                  80

gtg cag ggt cag cgc gta gcc agc acc ttt ttc cct aac tgg cgg gcc      288
Val Gln Gly Gln Arg Val Ala Ser Thr Phe Phe Pro Asn Trp Arg Ala
                 85                  90                  95

gga aag att acc gag ccg gct att gag gtg tcg ttg ggc ttc ggt atg      336
Gly Lys Ile Thr Glu Pro Ala Ile Glu Val Ser Leu Gly Phe Gly Met
                100                 105                 110

gac ggg atg ctc gcg gaa tac gtt gct ctg ccc tat gag gca acg ata      384
Asp Gly Met Leu Ala Glu Tyr Val Ala Leu Pro Tyr Glu Ala Thr Ile
                115                 120                 125

ccg ata ccg gag cac ctg tcg tac gag gag gct gca aca ttg cct tgc      432
Pro Ile Pro Glu His Leu Ser Tyr Glu Glu Ala Ala Thr Leu Pro Cys
        130                 135                 140

gcg gcg cta acc gct tgg aat gcg ttg acc gaa gtg ggg cgt gtc aag      480
Ala Ala Leu Thr Ala Trp Asn Ala Leu Thr Glu Val Gly Arg Val Lys
145                 150                 155                 160

gcc ggt gat acg gtc ttg ttg ctt ggc act ggc ggt gtc tcg atg ttc      528
Ala Gly Asp Thr Val Leu Leu Leu Gly Thr Gly Gly Val Ser Met Phe
                165                 170                 175

gcg ttg cag ttc gcc aag ctc ttg ggg gcg acg gtc att cac acc tcg      576
Ala Leu Gln Phe Ala Lys Leu Leu Gly Ala Thr Val Ile His Thr Ser
                180                 185                 190

agc agt gaa caa aag ctg gag agg gtg aaa gcg atg ggg gct gat cat      624
Ser Ser Glu Gln Lys Leu Glu Arg Val Lys Ala Met Gly Ala Asp His
                195                 200                 205

ctg atc aac tac cgc aat tcg cca ggg tgg gac cgt act gtc ctg gat      672
Leu Ile Asn Tyr Arg Asn Ser Pro Gly Trp Asp Arg Thr Val Leu Asp
        210                 215                 220

ctc acc gcg ggg cga ggg gtt gac ctg gta gtc gag gta ggg ggg gcg      720
Leu Thr Ala Gly Arg Gly Val Asp Leu Val Val Glu Val Gly Gly Ala
225                 230                 235                 240

ggg acc ttg gag cgc tca ctt cgt gcg gtc aag gta ggc ggt att gtc      768
Gly Thr Leu Glu Arg Ser Leu Arg Ala Val Lys Val Gly Gly Ile Val
                245                 250                 255

gcc acg att ggg cta gtg gct ggc gtt ggc ccg att gac cca ttg ccg      816
Ala Thr Ile Gly Leu Val Ala Gly Val Gly Pro Ile Asp Pro Leu Pro
                260                 265                 270

ctt atc tcc agg gct att cag ctc tcg ggc gtc tat gtc ggt tcc cgg      864
Leu Ile Ser Arg Ala Ile Gln Leu Ser Gly Val Tyr Val Gly Ser Arg
                275                 280                 285

gaa atg ttt ctc tca atg aac aaa gcc att gca tca gcc gaa atc aag      912
Glu Met Phe Leu Ser Met Asn Lys Ala Ile Ala Ser Ala Glu Ile Lys
```

```
cca gtg atc gat tgc tgc ttc ccc atc gac gag gtt gga gat gct tat    960
Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr
305                 310             315                 320

gag tac atg cgt agc ggc aat cac ctt ggc aaa gta gtt atc acg atc   1008
Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile
                325             330                 335

taa                                                                1011
```

<210> 20
<211> 336
<212> PRT
<213> Pseudomonas sp.

<400> 20
```
Met Lys Ala Tyr Glu Leu His Lys Ile Ser Glu Gln Val Glu Val Arg
  1               5                  10                  15

Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu
             20                  25                  30

Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu
          35                  40                  45

Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser
       50                  55                  60

Asp Gly Ala Gly Glu Ile Val Glu Val Gly Pro Gly Val Ser Ser Glu
 65                  70                  75                  80

Val Gln Gly Gln Arg Val Ala Ser Thr Phe Phe Pro Asn Trp Arg Ala
                85                  90                  95

Gly Lys Ile Thr Glu Pro Ala Ile Glu Val Ser Leu Gly Phe Gly Met
            100                 105                 110

Asp Gly Met Leu Ala Glu Tyr Val Ala Leu Pro Tyr Glu Ala Thr Ile
            115                 120                 125

Pro Ile Pro Glu His Leu Ser Tyr Glu Glu Ala Ala Thr Leu Pro Cys
       130                 135                 140

Ala Ala Leu Thr Ala Trp Asn Ala Leu Thr Glu Val Gly Arg Val Lys
145                 150                 155                 160

Ala Gly Asp Thr Val Leu Leu Leu Gly Thr Gly Gly Val Ser Met Phe
            165                 170                 175

Ala Leu Gln Phe Ala Lys Leu Leu Gly Ala Thr Val Ile His Thr Ser
            180                 185                 190

Ser Ser Glu Gln Lys Leu Glu Arg Val Lys Ala Met Gly Ala Asp His
            195                 200                 205
```

```
Leu Ile Asn Tyr Arg Asn Ser Pro Gly Trp Asp Arg Thr Val Leu Asp
    210                 215                 220
Leu Thr Ala Gly Arg Gly Val Asp Leu Val Val Glu Val Gly Gly Ala
225                 230                 235                 240
Gly Thr Leu Glu Arg Ser Leu Arg Ala Val Lys Val Gly Gly Ile Val
                245                 250                 255


Ala Thr Ile Gly Leu Val Ala Gly Val Gly Pro Ile Asp Pro Leu Pro
                260                 265                 270
Leu Ile Ser Arg Ala Ile Gln Leu Ser Gly Val Tyr Val Gly Ser Arg
                275                 280                 285
Glu Met Phe Leu Ser Met Asn Lys Ala Ile Ala Ser Ala Glu Ile Lys
    290                 295                 300
Pro Val Ile Asp Cys Cys Phe Pro Ile Asp Glu Val Gly Asp Ala Tyr
305                 310                 315                 320
Glu Tyr Met Arg Ser Gly Asn His Leu Gly Lys Val Val Ile Thr Ile
                325                 330                 335


<210> 21
<211> 1518
<212> DNA
<213> Pseudomonas sp.

<400> 21
tcaccgtcgt gatcgggatt ggaaattcgt gcgaggacag cggccacgta ccggcgccct 60

gaagggctgg aaggttggag tttcgttaag gtctggtacc cagcagccat ggagagcggc 120

ccttagccgg aatggcagct tgatggttgc cacgggacca gactggatgt cttgagtgtc 180

gagaattacc agatcgctgc gattttcatc gaggcgacca accacggtca gcaagtaccc 240

gtcaccttcg gcggcggtcg gacttctagg gacgaaggcc ggctcctggg ccgccgaggc 300

ttcgccggag taccagaggt cgtagtcacc tcggtggttg tcccagatgc cgagtgagtt 360

gtacgcgaat atcttctcgg cctgctgatg cgcaagtggt ttgcgtggat cgtccacccc 420

cataaagcca tagcggttgc attgcagggc gaacgaagaa tccatgattg gcatttccgc 480

aaagaaatcg tgtagccggg ttcgcttgat ctcgtcgctg ctgctatcga ggtcaatttc 540

ccaacgagtc aggcgtggta cggctttctc aggggcgaag ggttggtttt gtgagttggg 600

gaaggggaac ggcaggattt cactttccat aaggtcgata taaatcttgg ttccgacttc 660
```

```
ccaagcattc acaacatgaa atacccagag cgccggtgcc ttgagccagc gaatcagact 720

gccctggcgc ggcgcgagta cgccaatgta gctgcccagt tccggctccc acatataaat 780

tggctgtttc gccttgaggc gggacaggct gttggtggcc ggcataattg ggaaaatgga 840

ccaatttcgg gtaatggcaa agtcgtgcat gaatgcgcca tagggctgct caaaccaagt 900

ttcatgtgtc accttgccgt gcttgtcgac aatgtaatag gccatgtctg gagttgcttc 960

gcccttagct gccgaaccga agaacaacaa gtcacccgtt tccgggtcat attttggatg 1020

ggcggtgtgg gtttggctgg taacttggcc gtcgtagtcg aagtgtccgc gagtttcaag 1080

tgtacgagga tccagttcgt acggtaggcc gtcttccttc accgccagca ccttgccgtg 1140

atggctaatg atgcttgtat tggcaacggt gcggtctagt ccttttacac tggtgtcgtc 1200

ggtataggcg tttctgtaca tgccaaatag cgattttcgc gctagtcgtt cggccgtgaa 1260

tcgagcggtt ttaacccagc gactgatgaa gtcgacatga ccatcttcga agtggaaggc 1320

agaggccatt ccatctccat ctatgaaggt gtggaatttt tgtggggtaa cttgaggctc 1380

tggcgtatta cggtagaacg ttccatttat tgattttggg atttcgccgt caacctctag 1440

atcgaacaag tctgcctcta tacgggtggg gagaagtgtt cctactaatt gcgggtcgtt 1500

gcggttgaat ctcgccat                                               1518


<210> 22
<211> 505
<212> PRT
<213> Pseudomonas sp.

<400> 22
Met Ala Arg Phe Asn Arg Asn Asp Pro Gln Leu Val Gly Thr Leu Leu
  1               5                  10                  15

Pro Thr Arg Ile Glu Ala Asp Leu Phe Asp Leu Glu Val Asp Gly Glu
              20                  25                  30

Ile Pro Lys Ser Ile Asn Gly Thr Phe Tyr Arg Asn Thr Pro Glu Pro
          35                  40                  45

Gln Val Thr Pro Gln Lys Phe His Thr Phe Ile Asp Gly Asp Gly Met
      50                  55                  60

Ala Ser Ala Phe His Phe Glu Asp Gly His Val Asp Phe Ile Ser Arg
 65                  70                  75                  80

Trp Val Lys Thr Ala Arg Phe Thr Ala Glu Arg Leu Ala Arg Lys Ser
                  85                  90                  95

Leu Phe Gly Met Tyr Arg Asn Pro Tyr Thr Asp Asp Thr Ser Val Lys
             100                 105                 110
```

```
Gly Leu Asp Arg Thr Val Ala Asn Thr Ser Ile Ile Ser His His Gly
    115                 120             125

Lys Val Leu Ala Val Lys Glu Asp Gly Leu Pro Tyr Glu Leu Asp Pro
    130                 135             140

Arg Thr Leu Glu Thr Arg Gly His Phe Asp Tyr Asp Gly Gln Val Thr
145                 150             155                 160

Ser Gln Thr His Thr Ala His Pro Lys Tyr Asp Pro Glu Thr Gly Asp
                165             170             175

Leu Leu Phe Phe Gly Ser Ala Ala Lys Gly Glu Ala Thr Pro Asp Met
            180             185             190

Ala Tyr Tyr Ile Val Asp Lys His Gly Lys Val Thr His Glu Thr Trp
        195             200             205

Phe Glu Gln Pro Tyr Gly Ala Phe Met His Asp Phe Ala Ile Thr Arg
    210             215             220

Asn Trp Ser Ile Phe Pro Ile Met Pro Ala Thr Asn Ser Leu Ser Arg
225             230             235                 240

Leu Lys Ala Lys Gln Pro Ile Tyr Met Trp Glu Pro Glu Leu Gly Ser
            245             250             255

Tyr Ile Gly Val Leu Ala Pro Arg Gln Gly Ser Leu Ile Arg Trp Leu
        260             265             270

Lys Ala Pro Ala Leu Trp Val Phe His Val Val Asn Ala Trp Glu Val
    275             280             285

Gly Thr Lys Ile Tyr Ile Asp Leu Met Glu Ser Glu Ile Leu Pro Phe
    290             295             300

Pro Phe Pro Asn Ser Gln Asn Gln Pro Phe Ala Pro Glu Lys Ala Val
305             310             315                 320

Pro Arg Leu Thr Arg Trp Glu Ile Asp Leu Asp Ser Ser Ser Asp Glu
            325             330             335

Ile Lys Arg Thr Arg Leu His Asp Phe Phe Ala Glu Met Pro Ile Met
            340             345             350

Asp Ser Ser Phe Ala Leu Gln Cys Asn Arg Tyr Gly Phe Met Gly Val
        355             360             365

Asp Asp Pro Arg Lys Pro Leu Ala His Gln Gln Ala Glu Lys Ile Phe
    370             375             380

Ala Tyr Asn Ser Leu Gly Ile Trp Asp Asn His Arg Gly Asp Tyr Asp
385             390             395                 400

Leu Trp Tyr Ser Gly Glu Ala Ser Ala Ala Gln Glu Pro Ala Phe Val
            405             410             415
```

```
Pro Arg Ser Pro Thr Ala Ala Glu Gly Asp Gly Tyr Leu Leu Thr Val
        420                 425                 430

Val Gly Arg Leu Asp Glu Asn Arg Ser Asp Leu Val Ile Leu Asp Thr
        435                 440                 445

Gln Asp Ile Gln Ser Gly Pro Val Ala Thr Ile Lys Leu Pro Phe Arg
    450                 455                 460

Leu Arg Ala Ala Leu His Gly Cys Trp Val Pro Asp Leu Asn Glu Thr
465                 470                 475                 480

Pro Thr Phe Gln Pro Phe Arg Ala Pro Val Arg Gly Arg Cys Pro Arg
                485                 490                 495

Thr Asn Phe Gln Ser Arg Ser Arg Arg
                500                 505


<210> 23
<211> 951
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(948)
<223> gene = "ORF3"

<400> 23
atg aca act att cgg tgg cgg cgt atg tcc att cac tct gag ggg atc      48
Met Thr Thr Ile Arg Trp Arg Arg Met Ser Ile His Ser Glu Gly Ile
 1               5                  10                  15

act ctc gcg gat tcg ccg ctg cat tgg gcg cat acc ctg aat gga tca     96
Thr Leu Ala Asp Ser Pro Leu His Trp Ala His Thr Leu Asn Gly Ser
             20                  25                  30

atg cgt act cat ttc gaa gtc cag cgt ctt gag cgg ggt aga ggt gcc    144
Met Arg Thr His Phe Glu Val Gln Arg Leu Glu Arg Gly Arg Gly Ala
         35                  40                  45

tcc ctt gcc cga tct aga ttt ggc gcg ggt gag ctg tac agt gcc att    192
Ser Leu Ala Arg Ser Arg Phe Gly Ala Gly Glu Leu Tyr Ser Ala Ile
     50                  55                  60

gca cca agc cag gta ctt cgc cac ttc aac gac cag cga aat gct gat    240
Ala Pro Ser Gln Val Leu Arg His Phe Asn Asp Gln Arg Asn Ala Asp
65                  70                  75                  80

gag gct gag cac agc tat ttg att cag ata cga agt ggc gct ttg ggc    288
Glu Ala Glu His Ser Tyr Leu Ile Gln Ile Arg Ser Gly Ala Leu Gly
                85                  90                  95

gtt gca tcc ggc gga aga aag gtg atc ttg gca aat ggt gat tgc tcc    336
Val Ala Ser Gly Gly Arg Lys Val Ile Leu Ala Asn Gly Asp Cys Ser
```

```
                100                      105                      110

ata gtt gat agt cgc caa gac ttc aca ctt tcc tcg aac tct tcg acc    384
Ile Val Asp Ser Arg Gln Asp Phe Thr Leu Ser Ser Asn Ser Ser Thr
        115                  120                  125

caa ggt gtc gta ata cgc ttt ccg gtg agt tgg ctg gga gcg tgg gtg    432
Gln Gly Val Val Ile Arg Phe Pro Val Ser Trp Leu Gly Ala Trp Val
        130                  135                  140


tcc aat ccg gag gat ctt atc gcc cga cga gtt gat gct gag gta ggg    480
Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly
145                  150                  155                  160

tgg ggt agg gcg cta agc gca tcg gtt tct aat cta gat cca ttg cgc    528
Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg
                    165                  170                  175

atc gac gat tta ggt agc aat gta aat ggc att gca gag cat gtt gct    576
Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala
                180                  185                  190

atg tta att tca cta gca agt tct gcg gtt agt tct gaa gat ggg ggt    624
Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly
            195                  200                  205

gtg gct ctt cgg aaa atg agg gaa gtg aag aga gta ctc gag cag agt    672
Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser
        210                  215                  220

ttc gca gac gct aat ctc ggg ccg gaa agt gtt tca agt caa tta gga    720
Phe Ala Asp Ala Asn Leu Gly Pro Glu Ser Val Ser Ser Gln Leu Gly
225                  230                  235                  240

att tcg aaa cgc tat ttg cat tat gtc ttt gct gcg tgc ggt acg acc    768
Ile Ser Lys Arg Tyr Leu His Tyr Val Phe Ala Ala Cys Gly Thr Thr
                245                  250                  255

ttt ggt cgc gag ctg ttg gaa ata cgc ctg ggc aaa gct tat cga atg    816
Phe Gly Arg Glu Leu Leu Glu Ile Arg Leu Gly Lys Ala Tyr Arg Met
            260                  265                  270

ctc tgt gcg gcg agt gac tcg ggt gct gtg ctg aag gtg gcc atg tcc    864
Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser
        275                  280                  285

tca ggt ttt tcg gat tca agc cat ttc agc aag aaa ttt aag gaa aga    912
Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg
        290                  295                  300

tac ggt gtt tcg cct gtc tcc ttg gtg agg cag gct tga                951
Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala
305                  310                  315
```

<210> 24
<211> 316
<212> PRT
<213> Pseudomonas sp.

<400> 24
Met Thr Thr Ile Arg Trp Arg Arg Met Ser Ile His Ser Glu Gly Ile
 1   5   10   15

Thr Leu Ala Asp Ser Pro Leu His Trp Ala His Thr Leu Asn Gly Ser
                20   25   30

Met Arg Thr His Phe Glu Val Gln Arg Leu Glu Arg Gly Arg Gly Ala
            35   40   45

Ser Leu Ala Arg Ser Arg Phe Gly Ala Gly Glu Leu Tyr Ser Ala Ile
        50   55   60

Ala Pro Ser Gln Val Leu Arg His Phe Asn Asp Gln Arg Asn Ala Asp
65   70   75   80

Glu Ala Glu His Ser Tyr Leu Ile Gln Ile Arg Ser Gly Ala Leu Gly
                85   90   95

Val Ala Ser Gly Gly Arg Lys Val Ile Leu Ala Asn Gly Asp Cys Ser
            100   105   110

Ile Val Asp Ser Arg Gln Asp Phe Thr Leu Ser Ser Asn Ser Ser Thr
            115   120   125

Gln Gly Val Val Ile Arg Phe Pro Val Ser Trp Leu Gly Ala Trp Val
        130   135   140

Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly
145   150   155   160

Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg
            165   170   175

Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala
            180   185   190

Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly
        195   200   205

Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser
        210   215   220

Phe Ala Asp Ala Asn Leu Gly Pro Glu Ser Val Ser Ser Gln Leu Gly
225   230   235   240

Ile Ser Lys Arg Tyr Leu His Tyr Val Phe Ala Ala Cys Gly Thr Thr
            245   250   255

Phe Gly Arg Glu Leu Leu Glu Ile Arg Leu Gly Lys Ala Tyr Arg Met
            260   265   270

```
Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser
        275             280             285

Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg
        290             295             300

Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala
305                 310             315
```

<210> 25
<211> 735
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(732)
<223> product = "Enoyl-CoA-Hydratase" / gene = "ech"

<400> 25

```
atg agc cca act ctc aat cga gag atg gtc gag gtt ctg gag gtg ctg    48
Met Ser Pro Thr Leu Asn Arg Glu Met Val Glu Val Leu Glu Val Leu
 1               5              10                      15

gag cag gac gca gat gct cgc gtg ctt gtt ctg act ggt gca ggc gaa    96
Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu
                20              25              30

tcc tgg acc gcg ggc atg gac ctg aag gag tat ttc cgc gag acc gat   144
Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp
            35              40              45

gct ggc ccc gaa att ctg caa gag aag att cgt cgc gaa gcg tcg acc   192
Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr
    50              55              60

tgg cag tgg aag ctc ctg cgg atg tac acc aag ccg acc atc gcg atg   240
Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met
65              70              75                      80

gtc aat ggc tgg tgc ttc ggc ggc ggc ttc agc ccg ctg gtg gcc tgt   288
Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys
                85              90                      95

gat ctg gcc atc tgt gcc gac gag gcc acc ttt ggc ctg tcc gag atc   336
Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
            100             105             110

aac tgg ggc atc ccg ccg ggc aac ctg gtg agt aag gct atg gcc gac   384
Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
        115             120             125

acc gtg ggt cac cgc gag tcc ctt tac tac atc atg act ggc aag aca   432
```

```
Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr
    130                 135                 140

ttt ggc ggt cag cag gcc gcc aag atg ggg ctt gtg aac cag agt gtt    480
Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val
145                 150                 155                 160

ccg ctg gcc gag ctg cgc agt gtc act gta gag ctg gct cag aac ctg    528
Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu
                    165                 170                 175


ctg gac aag aac ccc gta gtg ctg cgt gcc gcc aaa ata ggc ttc aag    576
Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys
                    180                 185                 190

cgt tgc cgc gag ctg act tgg gag cag aac gag gac tac ctg tac gcc    624
Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala
            195                 200                 205

aag ctc gac caa tcc cgt ttg ctc gat ccg gaa ggc ggt cgc gag cag    672
Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln
        210                 215                 220

ggc atg aag cag ttc ctt gac gag aaa agc atc aag ccg ggc ttg cag    720
Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln
225                 230                 235                 240

acc tac aag cgc tga                                                 735
Thr Tyr Lys Arg


<210> 26
<211> 244
<212> PRT
<213> Pseudomonas sp.

<400> 26
Met Ser Pro Thr Leu Asn Arg Glu Met Val Glu Val Leu Glu Val Leu
  1               5                  10                  15

Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu
                20                  25                  30

Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp
            35                  40                  45

Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr
        50                  55                  60

Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met
65                  70                  75                  80

Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys
                85                  90                  95
```

```
Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
            100                 105                 110

Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
            115                 120                 125

Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr
    130                 135                 140

Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val
145                 150                 155                 160


Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu
                165                 170                 175

Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys
            180                 185                 190

Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala
        195                 200                 205

Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln
    210                 215                 220

Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln
225                 230                 235                 240

Thr Tyr Lys Arg
```

<210> 27
<211> 1446
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1443)
<223> product = Vanillin-Dehydrogenase" / gene = "vdh"

<400> 27

```
atg ttt cac gtg ccc ctg ctt att ggt ggt aag cct tgt tca gca tct     48
Met Phe His Val Pro Leu Leu Ile Gly Gly Lys Pro Cys Ser Ala Ser
  1               5                  10                  15

gat gag cgc acc ttc gag cgt cgt agc ccg ctg acc gga gaa gtg gta     96
Asp Glu Arg Thr Phe Glu Arg Arg Ser Pro Leu Thr Gly Glu Val Val
                20                  25                  30

tcg cgc gtc gct gct gcc agt ttg gaa gat gcg gac gcc gca gtg gcc    144
Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala
            35                  40                  45
```

```
gct gca cag gct gcg ttt cct gaa tgg gcg gcg ctt gct ccg agc gaa     192
Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu
         50              55                  60

cgc cgt gcc cga ctg ctg cga gcg gcg gat ctt cta gag gac cgt tct     240
Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser
 65              70                  75                  80

tcc gag ttc acc gcc gca gcg agt gaa act ggc gca gcg gga aac tgg     288
Ser Glu Phe Thr Ala Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp
                 85                  90                  95


tat ggg ttt aac gtt tac ctg gcg gcg ggc atg ttg cgg gaa gcc gcg     336
Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala
                 100                 105                 110

gcc atg acc aca cag att cag ggc gat gtc att ccg tcc aat gtg ccc     384
Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro
         115                 120                 125

ggt agc ttt gcc atg gcg gtt cga cag cca tgt ggc gtg gtg ctc ggt     432
Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly
         130                 135                 140

att gcg cct tgg aat gct ccg gta atc ctt ggc gta cgg gct gtt gcg     480
Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala
145                 150                 155                 160

atg ccg ttg gca tgc ggc aat acc gtg gtg ttg aaa agc tct gag ctg     528
Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu
                 165                 170                 175

agt ccc ttt acc cat cgc ctg att ggt cag gtg ttg cat gat gct ggt     576
Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly
                 180                 185                 190

ctg ggg gat ggc gtg gtg aat gtc atc agc aat gcc ccg caa gac gct     624
Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala
         195                 200                 205

cct gcg gtg gtg gag cga ctg att gca aat cct gcg gta cgt cga gtg     672
Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val
         210                 215                 220

aac ttc acc ggt tcg acc cac gtt gga cgg atc att ggt gag ctg tct     720
Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser
225                 230                 235                 240

gcg cgt cat ctg aag cct gct gtg ctg gaa tta ggt ggt aag gct ccg     768
Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro
             245                 250                 255

ttc ttg gtc ttg gac gat gcc gac ctc gat gcg gcg gtc gaa gcg gcg     816
Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala
             260                 265                 270
```

```
gcc ttt ggt gcc tac ttc aat cag ggt caa atc tgc atg tcc act gag      864
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu
        275                 280                 285

cgt ctg att gtg aca gca gtc gca gac gcc ttt gtt gaa aag ctg gcg      912
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala
        290                 295                 300

agg aag gtc gcc aca ctg cgt gct ggc gat cct aat gat ccg caa tcg      960
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser
305                 310                 315                 320


gtc ttg ggt tcg ttg att gat gcc aat gca ggt caa cgc atc cag gtt     1008
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val
                325                 330                 335

ctg gtc gat gat gcg ctc gca aaa ggc gcg cgg cag gtc gtc ggt ggt     1056
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly
                340                 345                 350

ggc tta gat ggc agc atc atg cag ccg atg ctg ctt gat cag gtc act     1104
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr
                355                 360                 365

gaa gag atg cgg ctc tac cgt gag gag tcc ttt ggc cct gtt gcc gtt     1152
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val
        370                 375                 380

gtc ttg cgc ggc gat ggt gat gaa gaa ctg ctg cgt ctt gcc aac gat     1200
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp
385                 390                 395                 400

tcg gag ttt ggt ctt tcg gcc gcc att ttc agc cgt gac gtc tcg cgc     1248
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg
                405                 410                 415

gca atg gaa ttg gcc cag cgc gtc gat tcg ggc att tgc cat atc aat     1296
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn
                420                 425                 430

gga ccg act gtg cat gac gag gct cag atg cca ttc ggt ggg gtg aag     1344
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys
                435                 440                 445

tcc agc ggc tac ggc agc ttc ggc agt cga gca tcg att gag cac ttt     1392
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe
        450                 455                 460

acc cag ctg cgc tgg ctg acc att cag aat ggc ccg cgg cac tat cca     1440
Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro
465                 470                 475                 480

atc taa                                                              1446
Ile
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<210> 28
<211> 481
<212> PRT
<213> Pseudomonas sp.

<400> 28
Met Phe His Val Pro Leu Leu Ile Gly Gly Lys Pro Cys Ser Ala Ser
 1   5   10   15

Asp Glu Arg Thr Phe Glu Arg Arg Ser Pro Leu Thr Gly Glu Val Val
                20   25   30

Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala
            35   40   45

Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu
        50   55   60

Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser
 65   70   75   80

Ser Glu Phe Thr Ala Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp
                85   90   95

Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala
            100   105   110

Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro
        115   120   125

Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly
        130   135   140

Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala
145   150   155   160

Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu
                165   170   175

Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly
            180   185   190

Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala
            195   200   205

Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val
        210   215   220

Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser
225   230   235   240

Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro
                245   250   255

```
Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala
        260                 265                 270

Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu
        275                 280                 285

Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala
        290                 295                 300

Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser
305                 310                 315                 320

Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val
                325                 330                 335

Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly
                340                 345                 350

Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr
                355                 360                 365

Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val
        370                 375                 380

Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp
385                 390                 395                 400

Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg
                405                 410                 415

Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn
                420                 425                 430

Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys
                435                 440                 445

Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe
        450                 455                 460

Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro
465                 470                 475                 480

Ile


<210> 29
<211> 1770
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1767)
<223> product = "Ferulasaeure-CoA-Synthetase" / gene =
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<400> 29
atg cgt tct ctc gag gcg ctt ctt ccc ttc ccg ggt cga att ctt gag    48
Met Arg Ser Leu Glu Ala Leu Leu Pro Phe Pro Gly Arg Ile Leu Glu
 1               5                   10                  15

cgt ctc gag cat tgg gct aag acc cgt cca gaa caa acc tgc gtt gct    96
Arg Leu Glu His Trp Ala Lys Thr Arg Pro Glu Gln Thr Cys Val Ala
            20                  25                  30

gcc agg gcg gca aat ggg gaa tgg cgt cgt atc agc tac gcg gaa atg   144
Ala Arg Ala Ala Asn Gly Glu Trp Arg Arg Ile Ser Tyr Ala Glu Met
        35                  40                  45


ttc cac aac gtc cgc gcc atc gca cag agc ttg ctt cct tac gga cta   192
Phe His Asn Val Arg Ala Ile Ala Gln Ser Leu Leu Pro Tyr Gly Leu
    50                  55                  60

tcg gca gag cgt ccg ctg ctt atc gtc tct gga aat gac ctg gaa cat   240
Ser Ala Glu Arg Pro Leu Leu Ile Val Ser Gly Asn Asp Leu Glu His
65                  70                  75                  80

ctt cag ctg gca ttt ggg gct atg tat gcg ggc att ccc tat tgc ccg   288
Leu Gln Leu Ala Phe Gly Ala Met Tyr Ala Gly Ile Pro Tyr Cys Pro
                85                  90                  95

gtg tct cct gct tat tca ctg ctg tcg caa gat ttg gcg aag ctg cgt   336
Val Ser Pro Ala Tyr Ser Leu Leu Ser Gln Asp Leu Ala Lys Leu Arg
            100                 105                 110

cac atc gta ggt ctt ctg caa ccg gga ctg gtc ttt gct gcc gat gca   384
His Ile Val Gly Leu Leu Gln Pro Gly Leu Val Phe Ala Ala Asp Ala
            115                 120                 125

gca cct ttc cag cgc gca att gag acc att ctg ccg gac gac gtg ccc   432
Ala Pro Phe Gln Arg Ala Ile Glu Thr Ile Leu Pro Asp Asp Val Pro
    130                 135                 140

gca atc ttc act cga ggc gaa ttg gcc ggg cgg cgc acg gtg agt ttt   480
Ala Ile Phe Thr Arg Gly Glu Leu Ala Gly Arg Arg Thr Val Ser Phe
145                 150                 155                 160

gac agc ctg ctg gag cag cct ggt ggg att gag gca gat aat gcc ttt   528
Asp Ser Leu Leu Glu Gln Pro Gly Gly Ile Glu Ala Asp Asn Ala Phe
                165                 170                 175

gcg gca act ggc ccc gat acg att gcc aag ttc ttg ttc act tct ggc   576
Ala Ala Thr Gly Pro Asp Thr Ile Ala Lys Phe Leu Phe Thr Ser Gly
            180                 185                 190

tct acc aaa ctg cct aag gcg gtg ccg act act cag cga atg ctc tgc   624
Ser Thr Lys Leu Pro Lys Ala Val Pro Thr Thr Gln Arg Met Leu Cys
            195                 200                 205
```

```
gcc aat cag cag atg ctt ctg caa act ttc ccg gtt ttt ggt gaa gag    672
Ala Asn Gln Gln Met Leu Leu Gln Thr Phe Pro Val Phe Gly Glu Glu
    210             215             220

ccg ccg gtg ctg gtg gac tgg ttg ccg tgg aac cac acc ttc ggc ggc    720
Pro Pro Val Leu Val Asp Trp Leu Pro Trp Asn His Thr Phe Gly Gly
225             230             235             240

agc cac aac atc ggc atc gtg ttg tac aac ggc ggc acg tac tac ctt    768
Ser His Asn Ile Gly Ile Val Leu Tyr Asn Gly Gly Thr Tyr Tyr Leu
            245             250             255

gac gac ggt aaa cca acc gcc caa ggg ttc gcc gag acg ctt cgc aac    816
Asp Asp Gly Lys Pro Thr Ala Gln Gly Phe Ala Glu Thr Leu Arg Asn
        260             265             270

ttg agc gaa atc tct ccc act gcg tac ctc act gtg ccg aaa ggc tgg    864
Leu Ser Glu Ile Ser Pro Thr Ala Tyr Leu Thr Val Pro Lys Gly Trp
        275             280             285

gag gaa tta gtg ggt gcc ctt gag cga gac agt acc ctg cgc gaa cgc    912
Glu Glu Leu Val Gly Ala Leu Glu Arg Asp Ser Thr Leu Arg Glu Arg
    290             295             300

ttc ttc gct cgc atg aag ctg ttc ttc ttc gcg gcg gct ggg ttg tcg    960
Phe Phe Ala Arg Met Lys Leu Phe Phe Phe Ala Ala Ala Gly Leu Ser
305             310             315             320

caa ggg atc tgg gat cgt ttg gac cgg gtc gct gaa cag cac tgt ggt    1008
Gln Gly Ile Trp Asp Arg Leu Asp Arg Val Ala Glu Gln His Cys Gly
            325             330             335

gag cgc att cgc atg atg gcg ggt ctg ggc atg acg gag act gct cct    1056
Glu Arg Ile Arg Met Met Ala Gly Leu Gly Met Thr Glu Thr Ala Pro
        340             345             350

tcc tgc act ttt acc acc gga ccg ctg tcg atg gct ggt tac att ggg    1104
Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly
        355             360             365

ctg cca gcg cct ggc tgc gag gtc aag ctc gtt ccg gtc gat ggg aaa    1152
Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys
        370             375             380

ttg gaa ggg cgt ttc cat ggt ccg cac gtc atg agc ggc tac tgg cgt    1200
Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg
385             390             395             400

gct cct gaa caa aat gcc caa gcg ttc gac gag gaa ggc tat tac tgc    1248
Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys
            405             410             415

tcc ggt gat gcc atc aaa ttg gca gat cct gcc gat cct cag aaa ggt    1296
Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly
            420             425             430
```

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ctg atg ttt gac ggt cga att gct gaa gac ttc aag ctg tcc tca ggg      1344
Leu Met Phe Asp Gly Arg Ile Ala Glu Asp Phe Lys Leu Ser Ser Gly
        435                 440                 445

gta ttt gtc agc gtt ggg cca ttg cgc acg cgg gcg gtt ctg gaa ggc      1392
Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly
        450                 455                 460

ggc tct tac gtc ctg gac gta gtg gtt gct gct cct gat cgt gaa tgc      1440
Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys
465                 470                 475                 480

ctt gga ttg ctc gtg ttt ccg cgt ctt ctc gac tgc cgt gcc ttg tcg      1488
Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser
                485                 490                 495


ggg cta gga aaa gag gcg tcg gac gcc gag gtg ctt gcc agt gag ccg      1536
Gly Leu Gly Lys Glu Ala Ser Asp Ala Glu Val Leu Ala Ser Glu Pro
                500                 505                 510

gtt cgg gcc tgg ttt gct gac tgg ctc aaa cga ctc aat cga gaa gca      1584
Val Arg Ala Trp Phe Ala Asp Trp Leu Lys Arg Leu Asn Arg Glu Ala
            515                 520                 525

act ggc aat gcc agt cgc atc atg tgg gta ggg ctc ctc gat acg ccg      1632
Thr Gly Asn Ala Ser Arg Ile Met Trp Val Gly Leu Leu Asp Thr Pro
        530                 535                 540

ccg tcg att gat aag ggc gag gtc act gac aag ggc tcg atc aac cag      1680
Pro Ser Ile Asp Lys Gly Glu Val Thr Asp Lys Gly Ser Ile Asn Gln
545                 550                 555                 560

cgc gct gtt ttg caa tgg cgg tcg gcg aaa gtt gat gcg ctg tat cgt      1728
Arg Ala Val Leu Gln Trp Arg Ser Ala Lys Val Asp Ala Leu Tyr Arg
                565                 570                 575

ggt gaa gat caa tcc atg ctg cgt gac gag gcc aca ctg tga              1770
Gly Glu Asp Gln Ser Met Leu Arg Asp Glu Ala Thr Leu
                580                 585
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<210> 30
<211> 589
<212> PRT
<213> Pseudomonas sp.

<400> 30

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Met Arg Ser Leu Glu Ala Leu Leu Pro Phe Pro Gly Arg Ile Leu Glu
  1               5                  10                  15

Arg Leu Glu His Trp Ala Lys Thr Arg Pro Glu Gln Thr Cys Val Ala
            20                  25                  30

Ala Arg Ala Ala Asn Gly Glu Trp Arg Arg Ile Ser Tyr Ala Glu Met
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Phe His Asn Val Arg Ala Ile Ala Gln Ser Leu Leu Pro Tyr Gly Leu
    50   55   60

Ser Ala Glu Arg Pro Leu Leu Ile Val Ser Gly Asn Asp Leu Glu His
65   70   75   80

Leu Gln Leu Ala Phe Gly Ala Met Tyr Ala Gly Ile Pro Tyr Cys Pro
                85   90   95

Val Ser Pro Ala Tyr Ser Leu Leu Ser Gln Asp Leu Ala Lys Leu Arg
            100   105   110

His Ile Val Gly Leu Leu Gln Pro Gly Leu Val Phe Ala Ala Asp Ala
            115   120   125

Ala Pro Phe Gln Arg Ala Ile Glu Thr Ile Leu Pro Asp Asp Val Pro
    130   135   140

Ala Ile Phe Thr Arg Gly Glu Leu Ala Gly Arg Arg Thr Val Ser Phe
145   150   155   160

Asp Ser Leu Leu Glu Gln Pro Gly Gly Ile Glu Ala Asp Asn Ala Phe
            165   170   175

Ala Ala Thr Gly Pro Asp Thr Ile Ala Lys Phe Leu Phe Thr Ser Gly
            180   185   190

Ser Thr Lys Leu Pro Lys Ala Val Pro Thr Thr Gln Arg Met Leu Cys
            195   200   205

Ala Asn Gln Gln Met Leu Leu Gln Thr Phe Pro Val Phe Gly Glu Glu
    210   215   220

Pro Pro Val Leu Val Asp Trp Leu Pro Trp Asn His Thr Phe Gly Gly
225   230   235   240

Ser His Asn Ile Gly Ile Val Leu Tyr Asn Gly Gly Thr Tyr Tyr Leu
            245   250   255

Asp Asp Gly Lys Pro Thr Ala Gln Gly Phe Ala Glu Thr Leu Arg Asn
            260   265   270

Leu Ser Glu Ile Ser Pro Thr Ala Tyr Leu Thr Val Pro Lys Gly Trp
            275   280   285

Glu Glu Leu Val Gly Ala Leu Glu Arg Asp Ser Thr Leu Arg Glu Arg
    290   295   300

Phe Phe Ala Arg Met Lys Leu Phe Phe Phe Ala Ala Ala Gly Leu Ser
305   310   315   320

Gln Gly Ile Trp Asp Arg Leu Asp Arg Val Ala Glu Gln His Cys Gly
            325   330   335

Glu Arg Ile Arg Met Met Ala Gly Leu Gly Met Thr Glu Thr Ala Pro

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                    340                    345                    350

Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly
        355                 360                 365

Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys
        370                 375                 380

Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg
385                 390                 395                 400

Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys
                405                 410                 415

Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly
            420                 425                 430

Leu Met Phe Asp Gly Arg Ile Ala Glu Asp Phe Lys Leu Ser Ser Gly
            435                 440                 445

Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly
        450                 455                 460

Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys
465                 470                 475                 480

Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser
                485                 490                 495

Gly Leu Gly Lys Glu Ala Ser Asp Ala Glu Val Leu Ala Ser Glu Pro
            500                 505                 510

Val Arg Ala Trp Phe Ala Asp Trp Leu Lys Arg Leu Asn Arg Glu Ala
            515                 520                 525

Thr Gly Asn Ala Ser Arg Ile Met Trp Val Gly Leu Leu Asp Thr Pro
        530                 535                 540

Pro Ser Ile Asp Lys Gly Glu Val Thr Asp Lys Gly Ser Ile Asn Gln
545                 550                 555                 560

Arg Ala Val Leu Gln Trp Arg Ser Ala Lys Val Asp Ala Leu Tyr Arg
            565                 570                 575

Gly Glu Asp Gln Ser Met Leu Arg Asp Glu Ala Thr Leu
            580                 585
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<210> 31
<211> 1296
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1293)

<223> product = "beta-Ketothiolase" / gene = "aat"

<400> 31
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atg agt tgg tca ggg ggg gct tac tcg gcg ttt tcc gac act gcg ttg      48
Met Ser Trp Ser Gly Gly Ala Tyr Ser Ala Phe Ser Asp Thr Ala Leu
 1               5                  10                  15

gtt gcg gca gtg cgc acc ccc tgg att gat tgc ggg ggt gcc ctg tcg      96
Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser
                20                  25                  30

ctg gtg tcg cct atc gac tta ggg gta aag gtc gct cgc gaa gtt ctg     144
Leu Val Ser Pro Ile Asp Leu Gly Val Lys Val Ala Arg Glu Val Leu
            35                  40                  45

atg cgt gcg tcg ctt gaa cca caa atg gtc gat agc gta ctc gca ggc     192
Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly
        50                  55                  60

tct atg gct caa gca agc ttt gat gct tac ctg ctc ccg cgg cac att     240
Ser Met Ala Gln Ala Ser Phe Asp Ala Tyr Leu Leu Pro Arg His Ile
 65                  70                  75                  80

ggc ttg tac agc ggt gtt ccc aag tcg gtt ccg gcc ttg ggg gtg cag     288
Gly Leu Tyr Ser Gly Val Pro Lys Ser Val Pro Ala Leu Gly Val Gln
                85                  90                  95

cgc att tgc ggc aca ggc ttc gaa ctg ctt cgg cag gcc ggc gag cag     336
Arg Ile Cys Gly Thr Gly Phe Glu Leu Leu Arg Gln Ala Gly Glu Gln
                100                 105                 110

att tcc caa ggc gct gat cac gtg ctg tgt gtc gcg gca gag tcc atg     384
Ile Ser Gln Gly Ala Asp His Val Leu Cys Val Ala Ala Glu Ser Met
            115                 120                 125

tcg cgt aac ccc atc gcg tcg tat aca cac cgg ggc ggg ttc cgc ctc     432
Ser Arg Asn Pro Ile Ala Ser Tyr Thr His Arg Gly Gly Phe Arg Leu
        130                 135                 140

ggt gcg ccc gtt gag ttc aag gat ttt ttg tgg gag gca ttg ttt gat     480
Gly Ala Pro Val Glu Phe Lys Asp Phe Leu Trp Glu Ala Leu Phe Asp
145                 150                 155                 160

cct gct cca gga ctc gac atg atc gct acc gca gaa aac ctg gcg cgc     528
Pro Ala Pro Gly Leu Asp Met Ile Ala Thr Ala Glu Asn Leu Ala Arg
                165                 170                 175

ctg tac gga atc acc agg gga gaa gct aat tcc tac gcg gta agc agc     576
Leu Tyr Gly Ile Thr Arg Gly Glu Ala Asn Ser Tyr Ala Val Ser Ser
                180                 185                 190

ttc gag cgc gca ttg agg gcg caa gag gag aaa tgg att gac caa gag     624
Phe Glu Arg Ala Leu Arg Ala Gln Glu Glu Lys Trp Ile Asp Gln Glu
            195                 200                 205

atc gtg gct gtt acg gat gaa cag ttc gat tta gag ggc tac aac agt     672
Ile Val Ala Val Thr Asp Glu Gln Phe Asp Leu Glu Gly Tyr Asn Ser
```

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cga gca att gaa ctg cct cgg aag gca aaa ttg ttg atc gtg aca gtc    720
Arg Ala Ile Glu Leu Pro Arg Lys Ala Lys Leu Leu Ile Val Thr Val
225                 230                 235                 240

atc cgc ggc cta gca gtc ttt gaa gcc ctt tcc cga ttg aag cct gtt    768
Ile Arg Gly Leu Ala Val Phe Glu Ala Leu Ser Arg Leu Lys Pro Val
                    245                 250                 255

cat tct ggc ggg gtg cag act gcg ggc aac agc tgt gcc gta gtg gac    816
His Ser Gly Gly Val Gln Thr Ala Gly Asn Ser Cys Ala Val Val Asp
                260                 265                 270

ggc gcc gcg gcg gct ttg gtg gct cga gag tcg tct gcg aca cag ccg    864
Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro
            275                 280                 285


gtc ttg gct agg ata ctg gct acc tcc gta gtc ggg atc gag ccc gag    912
Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu
        290                 295                 300

cat atg ggg ctc ggc cct gcg ccc gcg att cgc ctg ctg ctt gcg cgt    960
His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg
305                 310                 315                 320

agt gat ctt agt ttg agg gat atc gac ctc ttt gag ata aac gag gcg   1008
Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala
                    325                 330                 335

cag gcc gcc caa gtt cta gcg gta cag cat gaa ttg ggt att gag cac   1056
Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His
                340                 345                 350

tca aaa ctt aat att tgg ggc ggg gcc att gca ctt gga cac ccg ctt   1104
Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu
            355                 360                 365

gcc gcg acc gga ttg cgt ctc tgc atg acc ctc gct cac caa ttg caa   1152
Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln
        370                 375                 380

gct aat aac ttt cga tat gga att gcc tcg gca tgc att ggt ggg gga   1200
Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly
385                 390                 395                 400

cag ggg atg gcg gtt ctt tta gag aat ccc cac ttc ggt tcg tcc tct   1248
Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser
                    405                 410                 415

gca cga agt tcg atg att aac aga gtt gac cac tat cca ctg agc taa   1296
Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser
            420                 425                 430
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<210> 32
<211> 431
<212> PRT
<213> Pseudomonas sp.

<400> 32
Met Ser Trp Ser Gly Gly Ala Tyr Ser Ala Phe Ser Asp Thr Ala Leu
 1   5   10   15

Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser
            20   25   30

Leu Val Ser Pro Ile Asp Leu Gly Val Lys Val Ala Arg Glu Val Leu
        35   40   45

Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly
    50   55   60

Ser Met Ala Gln Ala Ser Phe Asp Ala Tyr Leu Leu Pro Arg His Ile
65   70   75   80

Gly Leu Tyr Ser Gly Val Pro Lys Ser Val Pro Ala Leu Gly Val Gln
                85   90   95

Arg Ile Cys Gly Thr Gly Phe Glu Leu Leu Arg Gln Ala Gly Glu Gln
            100   105   110

Ile Ser Gln Gly Ala Asp His Val Leu Cys Val Ala Ala Glu Ser Met
        115   120   125

Ser Arg Asn Pro Ile Ala Ser Tyr Thr His Arg Gly Gly Phe Arg Leu
    130   135   140

Gly Ala Pro Val Glu Phe Lys Asp Phe Leu Trp Glu Ala Leu Phe Asp
145   150   155   160

Pro Ala Pro Gly Leu Asp Met Ile Ala Thr Ala Glu Asn Leu Ala Arg
                165   170   175

Leu Tyr Gly Ile Thr Arg Gly Glu Ala Asn Ser Tyr Ala Val Ser Ser
                180   185   190

Phe Glu Arg Ala Leu Arg Ala Gln Glu Glu Lys Trp Ile Asp Gln Glu
            195   200   205

Ile Val Ala Val Thr Asp Glu Gln Phe Asp Leu Glu Gly Tyr Asn Ser
    210   215   220

Arg Ala Ile Glu Leu Pro Arg Lys Ala Lys Leu Leu Ile Val Thr Val
225   230   235   240

Ile Arg Gly Leu Ala Val Phe Glu Ala Leu Ser Arg Leu Lys Pro Val
                245   250   255

His Ser Gly Gly Val Gln Thr Ala Gly Asn Ser Cys Ala Val Val Asp
                260   265   270

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Gly Ala Ala Ala Ala Leu Val Ala Arg Glu Ser Ser Ala Thr Gln Pro
        275                 280                 285

Val Leu Ala Arg Ile Leu Ala Thr Ser Val Val Gly Ile Glu Pro Glu
        290                 295                 300

His Met Gly Leu Gly Pro Ala Pro Ala Ile Arg Leu Leu Leu Ala Arg
305                 310                 315                 320

Ser Asp Leu Ser Leu Arg Asp Ile Asp Leu Phe Glu Ile Asn Glu Ala
                325                 330                 335

Gln Ala Ala Gln Val Leu Ala Val Gln His Glu Leu Gly Ile Glu His
        340                 345                 350

Ser Lys Leu Asn Ile Trp Gly Gly Ala Ile Ala Leu Gly His Pro Leu
        355                 360                 365

Ala Ala Thr Gly Leu Arg Leu Cys Met Thr Leu Ala His Gln Leu Gln
        370                 375                 380

Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly
385                 390                 395                 400

Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser
                405                 410                 415

Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser
                420                 425                 430


<210> 33
<211> 1596
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1593)
<223> product = "Chemotaxis-Protein" / gene = "mac"

<400> 33
atg att agt ttc gct cgt atg gca gaa agt tta gga gtc cag gct aaa    48
Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys
  1               5                  10                  15

ctt gcc ctt gcc ttc gca ctc gta tta tgt gtc ggg ctg att gtt acc    96
Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr
            20                  25                  30

ggc acg ggt ttc tac agt gta cat acc ttg tca ggg ttg gtg gaa aag   144
Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys
        35                  40                  45

agc gcg ata gct ggt gag ttg cgg gcg aaa att cag gaa ctg aag gtt   192
Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val
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ctg gag cag cgc gcc tta ttc atc gcc gat gaa ggg tcg ctg aag cag   240
Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln
 65                      70                  75                  80

cgc tcg atc ctc cta agt cag gtg ata gct gaa gtt aat gat gct ata   288
Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile
                    85                  90                  95

gat att ttt gac ttt cag cgc gga cga tct gag tta ctt aaa ttc gct   336
Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala
                100                 105                 110

gct tct tcg cgc gaa gca agt tac tcc att gag gtc ggt agt aac gct   384
Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala
            115                 120                 125


gcg gcc gat aag ttg cag tcg ggc gaa cca agt gac gca ttg atg gtt   432
Ala Ala Asp Lys Leu Gln Ser Gly Glu Pro Ser Asp Ala Leu Met Val
        130                 135                 140

gcc gat aaa aag ctg aat gtt gag tat gag caa ttg agt tct gct gtg   480
Ala Asp Lys Lys Leu Asn Val Glu Tyr Glu Gln Leu Ser Ser Ala Val
145                 150                 155                 160

aat gca ctg atg ggg cat tta att gag gat cag aat gaa aaa gtt cca   528
Asn Ala Leu Met Gly His Leu Ile Glu Asp Gln Asn Glu Lys Val Pro
                165                 170                 175

cta atc tac tat atg ctt ggc ggc gta act ttg ttt acg atg ctc atg   576
Leu Ile Tyr Tyr Met Leu Gly Gly Val Thr Leu Phe Thr Met Leu Met
                180                 185                 190

agt gct tat tcg gtc tgg ttc att tcg cgt cag tta gtt ccg cca tta   624
Ser Ala Tyr Ser Val Trp Phe Ile Ser Arg Gln Leu Val Pro Pro Leu
            195                 200                 205

aag tcg acg gtg cag ctt gcc gag cgg att gca tca ggc gac ttg gct   672
Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala
        210                 215                 220

gat gtc ggg gac agc agg cgc aag gat gaa atc ggt cag ttg caa agt   720
Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser
225                 230                 235                 240

gca act agg cgg atg gcg att gga ctg cgt aat ctg gtc ggt gat att   768
Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile
                245                 250                 255

ggt caa agt cgt gcg caa ctg gtt tca tcg tcc agc gac ctt tcg gcc   816
Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala
                260                 265                 270

atc tgt gct cag gct cag att gat gtc gag tgc cag aag ctt tcg gtc   864
```

```
Ile Cys Ala Gln Ala Gln Ile Asp Val Glu Cys Gln Lys Leu Ser Val
        275                 280                 285

gcc cag gtc tct acc gcc gtg aac gag ttg gtt gaa acc gtc cag gca    912
Ala Gln Val Ser Thr Ala Val Asn Glu Leu Val Glu Thr Val Gln Ala
        290                 295                 300

ata gca aaa agc acc gaa gag gca gca aca gtc gcc gtc ttg gcc gat    960
Ile Ala Lys Ser Thr Glu Glu Ala Ala Thr Val Ala Val Leu Ala Asp
305                 310                 315                 320

gaa aag gca cgc ggt ggt gaa agt gtc gtt aac aag gcc gtt gat ttc    1008
Glu Lys Ala Arg Gly Gly Glu Ser Val Val Asn Lys Ala Val Asp Phe
                325                 330                 335

att gag cac ctc tcc gga gat atg gcg gaa ctg gga gac gca atg gag    1056
Ile Glu His Leu Ser Gly Asp Met Ala Glu Leu Gly Asp Ala Met Glu
                340                 345                 350


cgg ctt cag aac gac agt gcg cag atc aat aag gta gta gac gtc att    1104
Arg Leu Gln Asn Asp Ser Ala Gln Ile Asn Lys Val Val Asp Val Ile
                355                 360                 365

aag gct gtg gcg gag cag acc aat ctg cta gcc ctg aat gcg gcg ata    1152
Lys Ala Val Ala Glu Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile
        370                 375                 380

gag gcg gcc cgt gca gga gag cag ggc agg ggc ttt gcg gtc gtg gcg    1200
Glu Ala Ala Arg Ala Gly Glu Gln Gly Arg Gly Phe Ala Val Val Ala
385                 390                 395                 400

gat gag gtt cgt gct ttg gcg atg cgc acc caa caa tcg acc aaa gaa    1248
Asp Glu Val Arg Ala Leu Ala Met Arg Thr Gln Gln Ser Thr Lys Glu
                405                 410                 415

att gag agg cta gtg gtt tca ttg cag cag gga agt gaa gct gcg ggc    1296
Ile Glu Arg Leu Val Val Ser Leu Gln Gln Gly Ser Glu Ala Ala Gly
                420                 425                 430

gag ttg atg cgg cgt ggc aag gtc cgg acg cat gac gtc gtt gga ttg    1344
Glu Leu Met Arg Arg Gly Lys Val Arg Thr His Asp Val Val Gly Leu
                435                 440                 445

gcc cag caa gcc gcg cgc cgc gct act cga aat tac cca gct gtc gcc    1392
Ala Gln Gln Ala Ala Arg Arg Ala Thr Arg Asn Tyr Pro Ala Val Ala
        450                 455                 460

ggc atc caa gcg atg aac tat cag atc gcc gct gga gca gag cag caa    1440
Gly Ile Gln Ala Met Asn Tyr Gln Ile Ala Ala Gly Ala Glu Gln Gln
465                 470                 475                 480

ggg gct gct gtg gtt caa atc aac cag aat atg ctt gaa gtg cat aag    1488
Gly Ala Ala Val Val Gln Ile Asn Gln Asn Met Leu Glu Val His Lys
        485                 490                 495
```

```
atg gct gac gag tcc gcc att aaa gcg gga cag acc atg aag tca tcg    1536
Met Ala Asp Glu Ser Ala Ile Lys Ala Gly Gln Thr Met Lys Ser Ser
            500                     505                 510

aag gag ctt gct cac ctc ggc agt gcg cta caa aaa tcc gtt gat cga    1584
Lys Glu Leu Ala His Leu Gly Ser Ala Leu Gln Lys Ser Val Asp Arg
            515                     520                 525

ttc cag ctg tag                                                    1596
Phe Gln Leu
        530


<210> 34
<211> 531
<212> PRT
<213> Pseudomonas sp.

<400> 34
Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys
  1               5                  10                  15

Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr
                20                  25                  30

Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys
            35                  40                  45

Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val
        50                  55                  60

Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln
 65                  70                  75                  80

Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile
                85                  90                  95

Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala
            100                 105                 110

Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala
            115                 120                 125

Ala Ala Asp Lys Leu Gln Ser Gly Glu Pro Ser Asp Ala Leu Met Val
        130                 135                 140

Ala Asp Lys Lys Leu Asn Val Glu Tyr Glu Gln Leu Ser Ser Ala Val
145                 150                 155                 160

Asn Ala Leu Met Gly His Leu Ile Glu Asp Gln Asn Glu Lys Val Pro
                165                 170                 175

Leu Ile Tyr Tyr Met Leu Gly Gly Val Thr Leu Phe Thr Met Leu Met
            180                 185                 190

Ser Ala Tyr Ser Val Trp Phe Ile Ser Arg Gln Leu Val Pro Pro Leu
            195                 200                 205
```

```
Lys Ser Thr Val Gln Leu Ala Glu Arg Ile Ala Ser Gly Asp Leu Ala
    210             215             220

Asp Val Gly Asp Ser Arg Arg Lys Asp Glu Ile Gly Gln Leu Gln Ser
225             230             235             240

Ala Thr Arg Arg Met Ala Ile Gly Leu Arg Asn Leu Val Gly Asp Ile
            245             250             255

Gly Gln Ser Arg Ala Gln Leu Val Ser Ser Ser Ser Asp Leu Ser Ala
            260             265            ·270

Ile Cys Ala Gln Ala Gln Ile Asp Val Glu Cys Gln Lys Leu Ser Val
        275             280             285

Ala Gln Val Ser Thr Ala Val Asn Glu Leu Val Glu Thr Val Gln Ala
    290             295             300

Ile Ala Lys Ser Thr Glu Glu Ala Ala Thr Val Ala Val Leu Ala Asp
305             310             315             320

Glu Lys Ala Arg Gly Gly Glu Ser Val Val Asn Lys Ala Val Asp Phe
            325             330             335

Ile Glu His Leu Ser Gly Asp Met Ala Glu Leu Gly Asp Ala Met Glu
            340             345             350

Arg Leu Gln Asn Asp Ser Ala Gln Ile Asn Lys Val Val Asp Val Ile
    355             360             365

Lys Ala Val Ala Glu Gln Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile
    370             375             380

Glu Ala Ala Arg Ala Gly Glu Gln Gly Arg Gly Phe Ala Val Val Ala
385             390             395             400

Asp Glu Val Arg Ala Leu Ala Met Arg Thr Gln Gln Ser Thr Lys Glu
            405             410             415

Ile Glu Arg Leu Val Val Ser Leu Gln Gln Gly Ser Glu Ala Ala Gly
            420             425             430

Glu Leu Met Arg Arg Gly Lys Val Arg Thr His Asp Val Val Gly Leu
            435             440             445

Ala Gln Gln Ala Ala Arg Arg Ala Thr Arg Asn Tyr Pro Ala Val Ala
    450             455             460

Gly Ile Gln Ala Met Asn Tyr Gln Ile Ala Ala Gly Ala Glu Gln Gln
465             470             475             480

Gly Ala Ala Val Val Gln Ile Asn Gln Asn Met Leu Glu Val His Lys
            485             490             495

Met Ala Asp Glu Ser Ala Ile Lys Ala Gly Gln Thr Met Lys Ser Ser
            500             505             510
```

Lys Glu Leu Ala His Leu Gly Ser Ala Leu Gln Lys Ser Val Asp Arg
        515   520   525

Phe Gln Leu
    530

<210> 35
<211> 411
<212> DNA
<213> Pseudomonas sp.

<400> 35
ctagcctaac tgttgcgctt caggctccgc atggatcttg tgcagcagca atagcaattg 60

ttcacgttcg tcatcactca gcatcgacgt cgcgtcttgg tcgctctgta ccacgatctt 120

cttcagctct ttgagctgcg tctccccagc tttgctgaga aatatcccat aggaacgctt 180

gtccggcttg cagcgcacgc gcacagcaag gccgagcttc tcgagcttgt tcagcaaggg 240

aaccagttgt ggtggttcga ttgcgagcat ccgcgctagg tcagcctgca taagcccagg 300

gctcgcttcg atgattagaa gtgccgacag ctgcgccggg cgtaggtcat atggcgtcag 360

ggcttcaatc aggccctgag cgagcttcag ctgtgagccg gcgtaaggca t   411

<210> 36
<211> 136
<212> PRT
<213> Pseudomonas sp.

<400> 36
Met Pro Tyr Ala Gly Ser Gln Leu Lys Leu Ala Gln Gly Leu Ile Glu
  1   5   10   15

Ala Leu Thr Pro Tyr Asp Leu Arg Pro Ala Gln Leu Ser Ala Leu Leu
            20   25   30

Ile Ile Glu Ala Ser Pro Gly Leu Met Gln Ala Asp Leu Ala Arg Met
        35   40   45

Leu Ala Ile Glu Pro Pro Gln Leu Val Pro Leu Leu Asn Lys Leu Glu
    50   55   60

Lys Leu Gly Leu Ala Val Arg Val Arg Cys Lys Pro Asp Lys Arg Ser
65   70   75   80

Tyr Gly Ile Phe Leu Ser Lys Ala Gly Glu Thr Gln Leu Lys Glu Leu
                85   90   95

Lys Lys Ile Val Val Gln Ser Asp Gln Asp Ala Thr Ser Met Leu Ser
            100   105   110

```
Asp Asp Glu Arg Glu Gln Leu Leu Leu Leu Leu His Lys Ile His Ala
        115                 120                 125

Glu Pro Glu Ala Gln Gln Leu Gly
    130                 135


<210> 37
<211> 1446
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(1443)
<223> prodict = "Coniferylaldehyd-Dehydrogenase" / gene
      = "caldh"



<400> 37

atg agc att ctt ggt ttg aat ggt gcc ccg gtc gga gct gag cag ctg      48
Met Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu
  1               5                  10                  15

ggc tcg gct ctt gat cgc atg aag aag gcg cac ctg gag cag ggg cct      96
Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro
                20                  25                  30

gca aac ttg gag ctg cgt ctg agt agg ctg gat cgt gcg att gca atg     144
Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met
            35                  40                  45

ctt ctg gaa aat cgt gaa gca att gcc gac gcg gtt tct gct gac ttt     192
Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe
        50                  55                  60

ggc aat cgc agc cgt gag caa aca ctg ctt tgc gac att gct ggc tcg     240
Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser
 65                  70                  75                  80

gtg gca agc ctg aag gat agc cgc gag cac gtg gcc aaa tgg atg gag     288
Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu
                85                  90                  95

ccc gaa cat cac aag gcg atg ttt cca ggg gcg gag gca cgc gtt gag     336
Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu
                100                 105                 110

ttt cag ccg ctg ggt gtc gtt ggg gtc att agt ccc tgg aac ttc cct     384
Phe Gln Pro Leu Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro
            115                 120                 125

atc gta ctg gcc ttt ggg ccg ctg gcc ggc ata ttc gca gca ggt aat     432
Ile Val Leu Ala Phe Gly Pro Leu Ala Gly Ile Phe Ala Ala Gly Asn
        130                 135                 140
```

```
cgc gcc atg ctc aag ccg tcc gag ctt acc ccg cgg act tct gcc ctg    480
Arg Ala Met Leu Lys Pro Ser Glu Leu Thr Pro Arg Thr Ser Ala Leu
145             150                 155                 160

ctt gcg gag cta att gct cgt tac ttc gat gaa act gag ctg act aca    528
Leu Ala Glu Leu Ile Ala Arg Tyr Phe Asp Glu Thr Glu Leu Thr Thr
                165                 170                 175

gtg ctg ggc gac gct gaa gtc ggt gcg ctg ttc agt gct cag cct ttc    576
Val Leu Gly Asp Ala Glu Val Gly Ala Leu Phe Ser Ala Gln Pro Phe
            180                 185                 190

gat cat ctg atc ttc acc ggc ggc act gcc gtg gcc aag cac atc atg    624
Asp His Leu Ile Phe Thr Gly Gly Thr Ala Val Ala Lys His Ile Met
        195                 200                 205

cgt gcc gcg gcg gat aac cta gtg ccc gtt acc ctg gaa ttg ggt ggc    672
Arg Ala Ala Ala Asp Asn Leu Val Pro Val Thr Leu Glu Leu Gly Gly
    210                 215                 220

aaa tcg ccg gtg atc gtt tcc cgc agt gca gat atg gcg gac gtt gca    720
Lys Ser Pro Val Ile Val Ser Arg Ser Ala Asp Met Ala Asp Val Ala
225             230                 235                 240

caa cgg gtg ttg acg gtg aaa acc ttc aat gcc ggg caa atc tgt ctg    768
Gln Arg Val Leu Thr Val Lys Thr Phe Asn Ala Gly Gln Ile Cys Leu
                245                 250                 255

gca ccg gac tat gtg ctg ctg ccg gaa gaa tcg ctg gat agc ttt gtc    816
Ala Pro Asp Tyr Val Leu Leu Pro Glu Glu Ser Leu Asp Ser Phe Val
            260                 265                 270

gcc gag gcg acg cgc ttc gtg gcc gca atg tat ccc tcg ctt cta gat    864
Ala Glu Ala Thr Arg Phe Val Ala Ala Met Tyr Pro Ser Leu Leu Asp
        275                 280                 285

aat ccg gat tac acg tcg atc atc aat gcc cga aat ttc gac cgt ctg    912
Asn Pro Asp Tyr Thr Ser Ile Ile Asn Ala Arg Asn Phe Asp Arg Leu
    290                 295                 300

cat cgc tac ctg act gat gcg cag gca aag gga ggg cgc gtc att gaa    960
His Arg Tyr Leu Thr Asp Ala Gln Ala Lys Gly Gly Arg Val Ile Glu
305                 310                 315                 320

atc aat cct gcg gcc gaa gag ttg ggg gat agt ggt atc agg aag atc   1008
Ile Asn Pro Ala Ala Glu Glu Leu Gly Asp Ser Gly Ile Arg Lys Ile
                325                 330                 335

gcg ccc act ttg atc gtg aat gtg tcg gat gaa atg ctg gtc ttg aac   1056
Ala Pro Thr Leu Ile Val Asn Val Ser Asp Glu Met Leu Val Leu Asn
            340                 345                 350

gag gag atc ttt ggt ccg ctg ctc ccg atc aag act tat cgt gat ttc   1104
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Lys Thr Tyr Arg Asp Phe
        355                 360                 365
```

```
gac tcg gct atc gac tac gtc aac agc aag cag cga cca ctt gcc tcg     1152
Asp Ser Ala Ile Asp Tyr Val Asn Ser Lys Gln Arg Pro Leu Ala Ser
    370             375             380

tac ttc ttc ggc gaa gat gcg gtt gag cgt gag caa gtg ctt aag cgt     1200
Tyr Phe Phe Gly Glu Asp Ala Val Glu Arg Glu Gln Val Leu Lys Arg
385             390             395             400

acg gtt tcg ggc gcc gtg gtc gtg aac gat gtc atg agc cat gtg atg     1248
Thr Val Ser Gly Ala Val Val Val Asn Asp Val Met Ser His Val Met
            405             410             415

atg gat acg ctt cca ttt ggt ggt gtg ggg cac tcg ggg atg ggg gca     1296
Met Asp Thr Leu Pro Phe Gly Gly Val Gly His Ser Gly Met Gly Ala
            420             425             430

tat cac ggc att tat ggt ttc cga acc ttc agc cat gcc aag cct gtt     1344
Tyr His Gly Ile Tyr Gly Phe Arg Thr Phe Ser His Ala Lys Pro Val
            435             440             445

ctc gtg caa agt cct gtg ggt gag tcg aac ttg gcg atg cgc gca ccc     1392
Leu Val Gln Ser Pro Val Gly Glu Ser Asn Leu Ala Met Arg Ala Pro
    450             455             460

tac gga gaa gcg atc cac gga ctg ctc tct gtc ctc ctt tca acg gag     1440
Tyr Gly Glu Ala Ile His Gly Leu Leu Ser Val Leu Leu Ser Thr Glu
465             470             475             480

tgt tag                                                              1446
Cys


<210> 38
<211> 481
<212> PRT
<213> Pseudomonas sp.

<400> 38
Met Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu
  1             5               10              15

Gly Ser Ala Leu Asp Arg Met Lys Lys Ala His Leu Glu Gln Gly Pro
            20              25              30

Ala Asn Leu Glu Leu Arg Leu Ser Arg Leu Asp Arg Ala Ile Ala Met
            35              40              45

Leu Leu Glu Asn Arg Glu Ala Ile Ala Asp Ala Val Ser Ala Asp Phe
    50              55              60

Gly Asn Arg Ser Arg Glu Gln Thr Leu Leu Cys Asp Ile Ala Gly Ser
65              70              75              80

Val Ala Ser Leu Lys Asp Ser Arg Glu His Val Ala Lys Trp Met Glu
            85              90              95

Pro Glu His His Lys Ala Met Phe Pro Gly Ala Glu Ala Arg Val Glu
```

```
                100                      105                      110
Phe Gln Pro Leu Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro
        115                  120                  125

Ile Val Leu Ala Phe Gly Pro Leu Ala Gly Ile Phe Ala Ala Gly Asn
    130                  135                  140

Arg Ala Met Leu Lys Pro Ser Glu Leu Thr Pro Arg Thr Ser Ala Leu
145                  150                  155                  160

Leu Ala Glu Leu Ile Ala Arg Tyr Phe Asp Glu Thr Glu Leu Thr Thr
            165                  170                  175

Val Leu Gly Asp Ala Glu Val Gly Ala Leu Phe Ser Ala Gln Pro Phe
            180                  185                  190

Asp His Leu Ile Phe Thr Gly Gly Thr Ala Val Ala Lys His Ile Met
        195                  200                  205

Arg Ala Ala Ala Asp Asn Leu Val Pro Val Thr Leu Glu Leu Gly Gly
    210                  215                  220

Lys Ser Pro Val Ile Val Ser Arg Ser Ala Asp Met Ala Asp Val Ala
225                  230                  235                  240

Gln Arg Val Leu Thr Val Lys Thr Phe Asn Ala Gly Gln Ile Cys Leu
            245                  250                  255

Ala Pro Asp Tyr Val Leu Leu Pro Glu Glu Ser Leu Asp Ser Phe Val
            260                  265                  270

Ala Glu Ala Thr Arg Phe Val Ala Ala Met Tyr Pro Ser Leu Leu Asp
            275                  280                  285

Asn Pro Asp Tyr Thr Ser Ile Ile Asn Ala Arg Asn Phe Asp Arg Leu
        290                  295                  300

His Arg Tyr Leu Thr Asp Ala Gln Ala Lys Gly Gly Arg Val Ile Glu
305                  310                  315                  320

Ile Asn Pro Ala Ala Glu Glu Leu Gly Asp Ser Gly Ile Arg Lys Ile
            325                  330                  335

Ala Pro Thr Leu Ile Val Asn Val Ser Asp Glu Met Leu Val Leu Asn
        340                  345                  350

Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Lys Thr Tyr Arg Asp Phe
    355                  360                  365

Asp Ser Ala Ile Asp Tyr Val Asn Ser Lys Gln Arg Pro Leu Ala Ser
    370                  375                  380

Tyr Phe Phe Gly Glu Asp Ala Val Glu Arg Glu Gln Val Leu Lys Arg
385                  390                  395                  400

Thr Val Ser Gly Ala Val Val Val Asn Asp Val Met Ser His Val Met
```

Met Asp Thr Leu Pro Phe Gly Gly Val Gly His Ser Gly Met Gly Ala
        420   425   430

Tyr His Gly Ile Tyr Gly Phe Arg Thr Phe Ser His Ala Lys Pro Val
    435   440   445

Leu Val Gln Ser Pro Val Gly Glu Ser Asn Leu Ala Met Arg Ala Pro
    450   455   460

Tyr Gly Glu Ala Ile His Gly Leu Leu Ser Val Leu Leu Ser Thr Glu
465   470   475   480

Cys

<210> 39
<211> 1827
<212> DNA
<213> Pseudomonas sp.

<400> 39
ctatttgtct agtggtcggc gcgaaattcg ataagaaagc tgggcgcgag tgaggccgag 60

ccggcgggca gcttccgaga cattgccttt cacctggccc agagcatggc taatcatcgc 120

gtcctccact tcttgcagcg tcatcgcgct caggtccttt gagtcaagcg gcgagtcgat 180

tgtgctggtc ggtttggaga aggaagtact tgggctgcca gtttcctgtg gctgattatc 240

ttgagcggtg gccaggatgc cgctggcccc aatggagaac atcggttgag tcagtcgttc 300

accgctagtg aagaggtggc tcacgtcaat ggctccatcc tccggagcgc tgatgactcc 360

gcgctccacc aaattttgaa gctcccggat gtttcctgga aagtcgtagc caagcagggc 420

attggctgca cgtggagtga atccgctgac cacccggcta tgacgctgat tgaagcggtg 480

caggaaatag gtcatcagga ggggaatgtc ttccttcctc tctcgaagcg gcgggaggtg 540

gatcgggtaa acattgaggc ggaaaaaaag gtcctcgcgg aactcgccgc gctggacgcc 600

tgcgcgaaga tcgacattgg ttgcggctac cacacggacg tcaaccttga gtgtcctgct 660

tccgccaacc cgttcgacct ccgactcttg cagggcgcga gtaacttcc cttgggccac 720

gaggcttagc gtccctatct cgtcaaggaa tagtgtgccg cccgaagcgc gctcgaaccg 780

tcctgctcga gattgggtgg cgccggtaaa cgccccccgt tcgacgccga acaactcgga 840

ctccatcagg gtttcgggaa tacgtgcgca attgaccgca caaacgggc cgtcgtgtct 900

Asp Ala Ala Leu Leu Lys Glu Arg Phe Ser Asn Ala Asp Pro Leu Ser
        100   105   110

Leu Phe Ala Ala Gly Pro Asn Leu His Ser Leu Glu Gly Ala Val Arg
        115   120   125

Val Glu Pro Ile His Phe Asp Phe Asp Met Asp Leu Gly Thr Tyr Tyr
    130   135   140

Gly Glu Phe Leu Trp His His Ser Ser Glu Asp Asp Glu His Ile Ala
145   150   155   160

His Tyr Gly Ile Gly Thr Glu Pro Ala Cys Trp Thr Gln Thr Gly Tyr
                165   170   175

Ala Ile Gly Tyr Thr Ser Ala Leu Val Gly Arg Leu Ile Leu Tyr Arg
            180   185   190

Glu Val Glu Cys Arg Ser Thr Gly Ser Gln Ile Cys Arg Met Ile Gly
        195   200   205

Lys Pro Ala Glu Glu Trp Glu Asp Ala Glu Glu Asp Leu Ala Ala Leu
    210   215   220

Ser Ala Thr Ile Cys Arg Gln Pro Ser Thr Pro Gln Arg Arg Arg Thr
225   230   235   240

Gln Gln Gly Gln Arg Asn Thr Pro His His Ser Ala Ala Asp Ser Ser
            245   250   255

Thr Ala Ser Glu His Asp Met Val Gly Ile Ser Ser Ala Phe Asn Ala
        260   265   270

Ala Cys His Met Leu Lys Arg Val Ala Pro Thr Glu Ala Thr Val Leu
    275   280   285

Phe Thr Gly Glu Ser Gly Val Gly Lys Glu Met Phe Ala Arg Met Leu
    290   295   300

His Arg Ile Ser Pro Arg His Asp Gly Pro Phe Val Ala Val Asn Cys
305   310   315   320

Ala Arg Ile Pro Glu Thr Leu Met Glu Ser Glu Leu Phe Gly Val Glu
            325   330   335

Arg Gly Ala Phe Thr Gly Ala Thr Gln Ser Arg Ala Gly Arg Phe Glu
        340   345   350

Arg Ala Ser Gly Gly Thr Leu Phe Leu Asp Glu Ile Gly Thr Leu Ser
        355   360   365

Leu Val Ala Gln Gly Lys Leu Leu Arg Ala Leu Gln Glu Ser Glu Val
    370   375   380

Glu Arg Val Gly Gly Ser Arg Thr Leu Lys Val Asp Val Arg Val Val
385   390   395   400

```
Ala Ala Thr Asn Val Asp Leu Arg Ala Gly Val Gln Arg Gly Glu Phe
            405                 410                 415

Arg Glu Asp Leu Phe Phe Arg Leu Asn Val Tyr Pro Ile His Leu Pro
            420                 425                 430

Pro Leu Arg Glu Arg Lys Glu Asp Ile Pro Leu Leu Met Thr Tyr Phe
            435                 440                 445

Leu His Arg Phe Asn Gln Arg His Ser Arg Val Val Ser Gly Phe Thr
    450                 455                 460

Pro Arg Ala Ala Asn Ala Leu Leu Gly Tyr Asp Phe Pro Gly Asn Ile
465                 470                 475                 480

Arg Glu Leu Gln Asn Leu Val Glu Arg Gly Val Ile Ser Ala Pro Glu
                485                 490                 495

Asp Gly Ala Ile Asp Val Ser His Leu Phe Thr Ser Gly Glu Arg Leu
            500                 505                 510

Thr Gln Pro Met Phe Ser Ile Gly Ala Ser Gly Ile Leu Ala Thr Ala
    515                 520                 525

Gln Asp Asn Gln Pro Gln Glu Thr Gly Ser Pro Ser Thr Ser Phe Ser
    530                 535                 540

Lys Pro Thr Ser Thr Ile Asp Ser Pro Leu Asp Ser Lys Asp Leu Ser
545                 550                 555                 560

Ala Met Thr Leu Gln Glu Val Glu Asp Ala Met Ile Ser His Ala Leu
            565                 570                 575

Gly Gln Val Lys Gly Asn Val Ser Glu Ala Ala Arg Arg Leu Gly Leu
            580                 585                 590

Thr Arg Ala Gln Leu Ser Tyr Arg Ile Ser Arg Arg Pro Leu Asp Lys
    595                 600                 605
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<210> 41
<211> 768
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (1)..(765)
<223> product = "Coniferylalkohol-Dehydrogenase" / gene
      = "cadh"

<400> 41
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atg caa ctg acc aac aag aaa atc gtc gtc acc gga gtg tcc tcc ggt   48
Met Gln Leu Thr Asn Lys Lys Ile Val Val Thr Gly Val Ser Ser Gly
```

```
       1                5                    10                     15

atc ggt gcc gaa act gcc cgc gtt ctg cgc tct cac ggc gcc aca gtg    96
Ile Gly Ala Glu Thr Ala Arg Val Leu Arg Ser His Gly Ala Thr Val
             20                    25                    30

att ggc gta gat cgc aac atg ccg agc ctg act ctg gat gct ttc gtt   144
Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val
             35                    40                    45

cag gct gac ctg agc cat cct gaa ggc atc gat aag gcc atc tct cag   192
Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln
             50                    55                    60

ctg ccg gag aaa att gac gga ctc tgc aat atc gcc ggg gtg ccc ggc   240
Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly
 65                    70                    75                    80

act gcc gat cct cag ctc gtc gca aac gtg aac tac ctg ggt cta aag   288
Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys
                   85                    90                    95

tat ctg acc gag gca gtc ctg tcg cgc att caa ccc ggt ggt tcg att   336
Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile
                  100                   105                   110

gtc aac gtg tcc tct gtg ctt ggc gcc gag tgg ccg gcc cgc ctt cag   384
Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln
             115                   120                   125

ttg cat aag gag ctg ggg agt gtt gtt gga ttc tcc gaa ggc cag gca   432
Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala
             130                   135                   140

tgg ctt aag cag aat cca gtg gcc ccc gaa ttc tgc tac cag tat ttc   480
Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe
145                   150                   155                   160

aaa gaa gca ctg atc gtt tgg tct caa gtt cag gcg cag gaa tgg ttc   528
Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe
                  165                   170                   175

atg agg acg tct gta cgc atg aac tgc atc gcc ccc ggc cct gta ttc   576
Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe
                  180                   185                   190

act ccc att ctc aat gag ttc gtc acc atg ctg ggt caa gag cgg act   624
Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr
                  195                   200                   205

cag gcg gac gct cat cgt att aag cgc cca gca tat gcc gat gaa gtg   672
Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val
             210                   215                   220

gcc gcg gtg att gca ttc atg tgt gct gag gag tca cgt tgg atc aac   720
Ala Ala Val Ile Ala Phe Met Cys Ala Glu Glu Ser Arg Trp Ile Asn
225                   230                   235                   240
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ggc ata aat att cca gtg gac gga ggt ttg gca tcg acc tac gtg taa     768
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             20                  25                  30

Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val
         35                  40                  45

Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln
     50                  55                  60

Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly
 65                  70                  75                  80

Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys
                 85                  90                  95

Tyr Leu Thr Glu Ala Val Leu Ser Arg Ile Gln Pro Gly Gly Ser Ile
            100                 105                 110

Val Asn Val Ser Ser Val Leu Gly Ala Glu Trp Pro Ala Arg Leu Gln
        115                 120                 125

Leu His Lys Glu Leu Gly Ser Val Val Gly Phe Ser Glu Gly Gln Ala
    130                 135                 140

Trp Leu Lys Gln Asn Pro Val Ala Pro Glu Phe Cys Tyr Gln Tyr Phe
145                 150                 155                 160

Lys Glu Ala Leu Ile Val Trp Ser Gln Val Gln Ala Gln Glu Trp Phe
                165                 170                 175

Met Arg Thr Ser Val Arg Met Asn Cys Ile Ala Pro Gly Pro Val Phe
            180                 185                 190

Thr Pro Ile Leu Asn Glu Phe Val Thr Met Leu Gly Gln Glu Arg Thr
            195                 200                 205

Gln Ala Asp Ala His Arg Ile Lys Arg Pro Ala Tyr Ala Asp Glu Val
    210                 215                 220

Ala Ala Val Ile Ala Phe Met Cys Ala Glu Glu Ser Arg Trp Ile Asn
225                 230                 235                 240
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Ser Ala Leu Xaa
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